Access DB#

SEARCH REQUEST FORM

Scientific and Technical Information Center

Danisatar'a Full Nama:		Fx	aminer# ·		Date:		
Art Unit: Phone Nu	ımber 30		Serial Num	ber:			
Requester's Full Name: Art Unit: Phone Nu Mail Box and Bldg/Room Location:		Results	Format Prefer	red (circle):	PAPER	DISK	E-MAIL
If more than one search is submit	ted, please	prioritize s	earches in o	rder of ne	ed. ******	****	*****
Please provide a detailed statement of the so Include the elected species or structures, ke utility of the invention. Define any terms the known. Please attach a copy of the cover sh	earch topic, and ywords, synony nat may have a s	describe as sp ms, acronyms special meanir	ecifically as pos , and registry nu ig. Give examp	sible the sub mbers, and c	ject matter ombine wit	to be sea h the coi	rched. ncept or
Title of Invention:							
Inventors (please provide full names): .		100					
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Earliest Priority Filing Date:					***		
For Sequence Searches Only Please includ appropriate serial number.			ent, child, division	al, or issued p	atent numb	ers) along	with the
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Date Searcher Picked Up:	Bibliographic		Dr.Link				
Date Completed: 7/3/40	Litigation		Lexis/Nexis			.	
Searcher Prep & Review Time:	Fulltext		Sequence Systems				
Clerical Prep Time:	Patent Family		www/Internet _				
Online Time:	Other	*	Other (specify)				·
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PTO-1590 (1-2000)

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the regult being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDCP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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Pteryyota; Neoptera; Endopteryyota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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453 teaaeteagteaaeggttgagatteaetetgaetteeeeaatetaageegeggatgeaaa
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                                                                               503 CCYYYTCCYYXYYYYYYYTYTYCTYCYTYTCTYCTYCTTTYYYYYYTYTTYYYYYTTC
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Location/Qualifiers
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
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39.2%; Pred. No. 1.1e-05;
tive 65; Mismatches 123;
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/db_xref="taxon:7227"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP).

http://www.edgp.ebi.ac.uk..This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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                                                                                                                                                                                                                                                                                                                                                                                              191 tttaatttcttaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaa
                                                                                          6.3%; Score 82.8; DB 123; Length 1101;
11arity 33.6%; Pred; No. 2.2e-05;
Conservative 90; Mismatches 133; Indels 0;
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/clone="BACN15C13"
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/clone="BACN16D22"
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                                203
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                                                                                                                              113;
                                                                                                             Best Local S
Matches 11
                                                                                                 Query Match
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CNS016E1/c
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KEYWORDS
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AUTHORS
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JOURNAL
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centred Fitude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                 1070 ATTITIWATITITITAMITMNINATITITIWAAMITITITITATITITAWAATAWITITIT 1011
                                                                                                                                                  1190 MAMAMAMMMHMTCTTTTTTTTTATAAAAAAWATTWTTTTTTTTTTTTTAAWC 1131
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                                                                                                                                                                                                                                                                                                                                                                                                      245
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                                                    Gaps
                                                                                                8 caaactcacatccaaacataacatggatatctccttaccaatcatactaattattttggg 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 26-JUL-1999
sequence T7 end of BAC
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                                                                                                                                                                                                       atgtataaaattatattattcatgatttttcatacatttgattttgataataa..atata
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1043)
Length 1201;
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                                                 Indels
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  DB 123;
                                                    46; Mismatches 121;
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Pred. No. 4.5e-05;
                               1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNSU145P 1043 bp DNA Drosphila melanogaster genome survey : BACN1011 of DrosBAC library from Drost fly), genomic survey sequence.
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     Score 81.2;
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                       Pred. No.
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/plasmid-"pBeloBAC11"
/db_xref-"taxon:7227"
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/clone="BACN11G11"
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  6.2%;
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Query Match 6.2
Best Local Similarity 44.8
Matches 137; Conservative
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 Conservative
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 Matches 115;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence T7 end of BAC BACN15E04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                       667
                                                                                                                                                                        tttcatacatttgattttgataataaatatatttttttaatttcppaaaaatgttgca 214
                                                                                                                                                                                                                                                                 tggcattgaaacgagagaaagagagtcagaaccagaagacaaataaaagtatgcaacaa 392
                                                                                                                                                                                                                                                                                                                                                                                                          TTTTWTWTATATTATWWTWTWTWAAAATATTTTTTATWTATATTTATWTATWTATWWA 727
                                                                                                                                                                                                                                             agacacttattagacatagtcttgttctgtttacaaaagcattcatcattaatacatta 274
                                                                   TCTTTTTTTTTATATAWATAWWTATWTATATAAAATAWTATATATATATTTTTATATATATWA 607
                                                                                                      attaattaagaaattaaaaagattttttaaaaaaatgtataaaaattatattcatgatt 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1999
T7 end of BAC
 Gaps
                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
1 (bases 1 to 1200)
                                                                                                                                       608 AAWAATATWTATATWTTTTTTTWWTWTWTTTATWTWWWAAATATATWTTTTTWTWTWT
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Mismatches 158; Indels
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/db_xref="taxon:7227"
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 58;
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 Conservative
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908 MCWAATHAWAA 918
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DEFINITION
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KEYWORDS
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TITLE
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Per 19 1900 and the Name of the Mail of Sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library fruitfly.org The BDGP Drosophila melanogaster BAC library days prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter da Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
   Drosophila melanogaster genome survey sequence T7 end of BAC # BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                             Sukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Uscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 928)
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29.7%; Pred. No. 0.00011;
iive 99; Mismatches 116;
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/db_xref="taxon:7227"
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/clone="BACR27A24"
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                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                            GI:4948170
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Length 1200;

Score 79.8; DB 123; Pred. No. 7.3e-05;

6.18;

Best Local Similarity

Query Match

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Matches 116;
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.frultfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BOGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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Muscomorpha; Ephydroldea; Drosophilidae; Drosophila
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Score 77.6; DB 122; Length 1101; Pred. No. 0.00018;

5.9%;

Query Match Best Local Similarity

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L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Gebranation of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pleter de Jong's Laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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tive 34; Mismatches 152;
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Lubrited (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

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Pterygota; Weoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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BP 191-91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                       1069 ATATAAAWTAWTATATTATATTWTATATATATATATTTTATWTTTATATATATATAT 1010
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/organism="brosophila melanogaster"
/plasmid="pBeloBAC11"
/db.xref="taxon:7227"
/clone_lib="brosBAC"
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Length 1101;

Score 76.8; DB 122; Pred. No. 0.00024;

5.88;

Query Match Best Local Similarity

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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence T7 end of BAC: BAC29993 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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949 WITWYITITITWITITAIMTWWIAWIIWWIIAAIAWIITITITWIWAIAIACAIWIIAIWI 890
                                                                                                                                                                                                                                                             tttttaatttcttaaaaaatgttgcaagacacttattagacatagtcttgttctgtttac 248
                                                                                                                                                      Eukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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36.0%; Pred. No. 0.00039;
Live 71; Mismatches 180; Indels 0;
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/clone_lib="RPCI-98"
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Web: www.genoscope.cns.fr.

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Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please 'see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2, cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR04A23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                               197 ttcttaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcat 256
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                                                                                               702 AAAAWATWAAWAATWATAWATAAWITAAAAWAATAAAAWAAWAATWAWATAATATWWAT 761
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 1101)
                                             522 TWITIWAWWIWIAWIAAAAAAAAWAIAAITIAAAWWAAIAWAITAAWAAIITAWAAWWI
109 others
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence.
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Drosophila melanogaster
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Score 75; DB 122; Length 1101; Pred. No. 0.0005;

5.78;

Best Local Similarity

Query Match

462 WIMMMMMWWAATWTWWAAWAAMTTATWAATWAAAAWAWWWMATTTTTWWWWTWAT 521

17 atccaaacataacatggatatctccttaccaatcatactaattattttgggttaaatatt 76

Best Local Similarity 36.08 Matches 141; Conservative

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Matches 129;

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Submitted (02-JUN-1999) Genoscope – Centre National de Sequencage
BP 191 91006 EVRY cedex – FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL071063
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                                                                                                                                              557 TWITTITITITITAWITITIAWITITIANITATWITAWITAAAWWIAWWAITITIATAWIWAATA 616
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Location/Qualifiers
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilldae, Drosophla.
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Length 928;
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Score 74.6; DB 122;
Pred. No. 0.00059;
                                                     91; Mismatches 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanogaster MAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial scorn digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence T7 end of BAC # $ASCR27A24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                       901 TWAAAAATAATAWAATAWWAAATTAAWAAAATAWATWAAAAAWNTAWWTATAAWTTWA 842
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 928
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/db_xref="taxon:7227"
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VERSION KEYWORDS SOURCE ORGANISM

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REFERENCE AUTHORS TITLE JOURNAL

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DEFINITION

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FEATURES

BASE COUNT ORIGIN

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Search completed: September 2, 2000, 00:24:41 Job time: 4305 sec 36,986

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UB-457-364-36 US-08-456-262-36 US-08-456-240-7

Sequence Sequence Sequence

5-416-36

Sequence Sequence Sequence

ALIGNMENTS

Sequence Sequence Sequence

PCT-US92-01385-2 CT-US92-01385-4

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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INTENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTONNEY, FAGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
TREFERROEAFORTEN NUMBER: 30472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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Patent No. 5670367
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 22313-0299
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September 1, 2000, 23:40:36 ; Search time 111.97 Seconds (without alignments) 1614.257 Million cell updates/sec
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Sequence 14
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-883-795A-36
US-08-446-855A-1
US-08-731-722-3
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US-08-883-795A-36
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US-08-910-551B-1
US-08-909-425A-1
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 1000000
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No.
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30472/114 IMMU

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LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                      linear
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ZIP: 32606-6669
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                                                                  MOLECULE TYPE:
                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                      ; ANTI-SENSE:
US-08-487-826B-13
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                                                      TOPOLOGY:
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Wellens, Thomas E.
YENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
VENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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              Length 7218;
                                                Conservative 241; Mismatches 136; Indels
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16th Floor
              Score 78; DB 1;
Pred. No. 7.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1431 YYYYGTACCAAATTCTTCTATCTTTTAACTA 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: NIH121.001CP1 PLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           914 atgagaaataaaatcattttttttttatttcaa 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         620 Newport Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knobbe Martens Olson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08487826B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller, Louis H
                                3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                    15;
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                                                    Matches
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1444 TTAGTATTTTAATAATAAATCTTTTAAAAACTTCAAAACATTTTTGCATAAAATA 1503
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                                                                                                                                                                                                    1264 ATTATAATATGTAAATTATTAATAAATATATTTGTATAACATACAAGACTAAAGAAAC 1323
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                                                                                                                                                                                                                                                                        117 tttttaaaaaaatgtataaaaattatattcatgatttttcatacatttgattttgata 176
                                                                                                                                       57 attattttgggttaaatattaatcattatttttaagatattäättaagaaattaaagat 116
                                                                                                                                                                                                                                                                                                                                                                                                               177 ataaatatattttttttaatttottaaaaaaatgttgoaagacaottattagacatagtot
   Length 19124;
Score 56; DB 4; Length 191
Pred. No. 0.012;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1564 ATTAGAACAAAAGAATATTACAAAAAATAATAAATTAAATTA 1607
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Best Local Similarity 47.7%;
Matches 164; Conservative
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TITLE OF INVENTION: Biocontrol of Fungal Soilborne Pathogens TITLE OF INVENTION: by Pythium oligandrum
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/731,723
                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
Sequence 5, Application US/08731722
Patent No. 5961971
                                                                                                                                                                                                                                                                                                                                                                         : Floppy disk
IBM PC compatible
                                                GENERAL INFORMATION:
APPLICANT: Martin, Frank N.
                                                                                                                                                                                                Saliwanchik &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,9
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
      linear
                                                    2
                    TYPE:
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                               HYPOTHETICAL:
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                                                  ANTI-SENSE:
US-08-487-826B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tt 1299
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                                                                                                                    Query Match
Best Local Simi
Matches 221;
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APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         535 ATCATTATTTAAAAATATAAATAAAAGTTT----TTCAATATTTATAATAAAATATATTC 480
                                                                                                                                                                                                                                                                                                                                                                                                          595 TATTGAAGAATTCTTATAACTACTATTAAAGATTTATAGGATCTACTGTATAAATCCAG 536
                                                                                                                                                                                                                                                                                                          112 aagattttttaaaaaaatgtataaaaattatattcatgattttccatacatttgattt 171
                                                                                                                                                                    Length 1186;
                                                                                                                                                                  Score 54.2; DB 4; Length 1.
Pred. No. 0.018;
0; Mismatches 73; Indels
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: 620 Newport Center Drive 16th Floor
Newport Beach
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NAME: ISTAELSEN, Ned
REGISTRATION UNBER: 29,655
REFERENCE/COCKET NUMBER: MIH121.001CP1
PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
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; Sequence 13, Application US/08487826B
; Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
ORMATION FOR SEQ ID NO: 13:
                                                  linear
:: DNA (genomic)
                                                                                                                                                                         4.1%;
                                                                                                   ; INDIVIDUAL ISOLATE: 23-5
US-08-731-722-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sim, Kim L.
Chitnis, Chetan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19124 base pairs
LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                     Query Match 4.13
Best Local Similarity 59.33
Matches 112; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 AAATTAATT 411
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                                                  TOPOLOGY: line
MOLECULE TYPE: I
ORIGINAL SOURCE:
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15820 TATIT -- AAATAAATITITITITATTITATGIATATITITITITITAACATITITIAAT 15763
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                                                                                                                                                                                                                                                              tatttcaaaataaaccttgggccttgtgctgactgagatggggtttggtgattacagaat 997
                                                                                         818 tgaaactctactctttctttaatatctgcggaatacgcgttggactttcagatctagtcg 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1178 gaaacttttgctttaaattctattataacttttttatggcaaaaatttttgcatgtgtc
                                                                                                                                                                           878 aaatcatttcataattgcctttctttttagcttatgagaaataaaatcattttttt
    Length 19124;
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Vectors for Tissue Plasminogen Activator
39
                                              Indels
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    Score 53:6; DB 4;
Pred. No. 0.033;
0; Mismatches 259;
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27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/08883795A
Patent No. 5985607
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA
TITLE OF INVENTION: Vectors for Tiss
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BERESKIN & PARR STREET: 40 King Street West CITY: Toronto
4.1%;
1 Similarity 45.9%;
221; Conservative 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
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NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: O'Sullivan, William J
FITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
FITLE OF INVENTION: phosphate synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 gcattcatcatttaatacattaaaaaaatatttaatactaacagta 297
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1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                        Score se.v.
Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08446855A Patent No. 5849573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REGISTRATION NUMBER: 40,26
REFERENCE/DOCKET NUMBER: 7
TELECOMMUNICATION INFORMATION
                                                          (416) 364-7311
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 55.1%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTORNEY/AGENT INFORMATION:
                                                                            TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 DASE PAIRS
                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   URRENT APPLICATION DATA
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                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                             linear
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                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                             MOLECULE TYPE:
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                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                          JS-08-883-795A-36
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111 aaagattttttaaaaaaatgtatäaaaattatattettcatgatttttcatacatttgatt 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 tagtottgttotgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatact 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                Biocontrol of Fungal Soilborne Pathogens by Pythium oligandrum
                                                                                                                                                                                                                                                       Score 52; DB 3; Length 8920;
Pred. No. 0.059;
                                                                                                                                                                                                                                                                                              0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 aacagtagaatcttcttgtgagtggtgt 318
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Patent No. 5961971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
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NFORMATION
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.6%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frank N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,
                                                                                                                   nucleic acid
EDNESS: single
                                                            INFORMATION FOR SEQ ID NO
                                                                             SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Martin,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32606-6669
                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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                                                                                                                                                                                                US-08-446-855A-1
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Martin, Frank N.
TITLE OF INVENTION: Biocontrol of Fungal Soilborne Pathogens
TITLE OF INVENTION: by Pythium oligandrum
                                                                                                                                                                         Length 3933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               683 GTAGAATTGAGAGAAATAAATACTTCTAATTTACTTTATATTAATAT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 gtottgttctgtttacaaaagcattcatcatttaatacattaaaaaatat 282
                                                                                                                                                                           3.9%; Score 51.2; DB 4; Length 3 54.3%; Pred. No. 0.076; W tive 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/731,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08731722
Patent No. 5961971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFRENCE/DOCKET NUMBER: UF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                     : OLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: 1986-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
3933 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3933 base pairs
                                                                                                                                                                                         Best Local Similarity 54.3 Matches 125; Conservative
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ZIP: 32606-6669
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                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-731-722-3/c
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113 agattttttaaaaaaatgtataaaaattataattattcatgatttttcatacatttgatttt 172
                                                            173 gataataaatatattttttttaatttcttaaaaaatgttgcaagacacttattagacata 232
 Length 3933;
                                                                                                                                                                                                                                                           3251 GTAGAATTGAGAGAAATAAATACTTCTAATTTACTTTATATTAATAATAT 3202
                                                                                                                                                                                                                                             233 gtcttgttctgtttacaaaagcattcatcatttaatacattaaaaaatat 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 665;
 Score 51.2; DB 4; Length 3 Pred. No. 0.076; 0; Mismatches 103; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 4
Pred. No. 0.066
                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/08883795A
Patent No. 5985607
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant
TITLE OF INVENTION: Vectors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
   3.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (416) 364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 665 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Query Match
Best Local Similarity
Matches 125; Conserva
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Best Local Similarity
Matches 131; Conserv
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ORIGINAL SOURCE:
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US-08-883-795A-36
                                                                                                                                                                                                                                                                                                                  RESULT 9
US-08-883-795A-36/c
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; NAME/KEY:
; LOCATION:
US-08-229-393-1
                                                                                                                                                                                                                                                508 TAATTATAAATACTTTAATTATAAAATATGTAATTATAAAATACTTTATAAAATATGTAAT 449
                                                                                                                                                                         ttttgataataaatatatttttttaatttcttaaaaaaatgttgcaagacacttattaga 228
                                                                                                                                                                                                            388 TATAAAATATGTAATTATAAACATTTTAATTATAAATATGTAATT$$PAACATTTTAAT 329
                     taaaagattttttaaaaaaatgtataaaaattatattettcatgattttcatacatttga 168
                                                                                                                                 448 TATAAAATATGTAATTATAAACATTTTAATTATAAAATATGTAATTATAAACATTTTAAT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F: Jenkins, Mark C
F: Fayer, Ronald
F: Tilley, Michael
F: Upton, Steven J
INVENTION: DNA Sequence Encoding Surface Protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Cryptosporidium Parvum
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1815 N. University Street
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IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08229393
Patent No. 5591434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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STREET: 10.
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CLONE: CP15/60
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APPLICANT
TITLE OF
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                                                                                                                                                                                      420 CGAATTATTAAAGAAAAGGGGAATACAGTTTCCTGATTCTTTGAGATGAATTGCAACACA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 ATTGTCGGAATCGCTGATTCCAGCACTACTTTCAACTCTAGAAAGCTCTTCCTTTGAATA 301
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                                                                                                                                                                                                                                 600 TITITITITITITAATCAAAATATTTTATTAATTCTCTCCCTGTGATTGAAGAAAA 541
                                                                                                                                                                                                                                                                                                                          540 GCTATITIGGATITIATIATAGGGTTTGGAAAAAAAAAATCCAGAATTAATGAAATTCCT 481
                                                                                                                                                                                                                                                                                                                                                                                                                   480 GITITAGITAAAGITIGGITIGAATITGITIGCIGITGCAACAAAICITICTITGICITG 421
                                                                               3; DB 1; Length 602; 0.071;
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                                                                                                                                         0; Mismatches 197; Indels
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                                                                                             Score 50.8;
pred. No. 0.
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APPLICATION NUMBER: GB 9206016.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Sandoz Agro, Inc
975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goldbach, Robert W. TITLE OF INVENTION: Improvemen TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                        3.9%;
nilarity 46.2%;
Conservative 0
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                           Query Match
Best Local Similarity
Matches 169; Conserva
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us-09-464-528-6.rni

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1233 AAAACCAAAAAATTTTTTTTTTAAATAAATAAGGCTCCGGCCAGATTTGGTCTAAGACC 1292
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                                                                                                                                                                                                                                                                                                                            Length 4970;
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Patent No. 5773700
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: van Grinsven J., Martinus Q.
APPLICANT: De Haan, Petrus T.
APPLICANT: Gielen L., Johannes J.
APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic
TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                          Query Match 3.8%; Score 50.2; DB 2; Length 49 Best Local Similarity 52.1%; Pred. No. 0.12; Matches 112; Conservative 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1413 CAATCATTCTGCCTTATTTAAAACACATTT 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 08/032,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB 9206016.9
                                  5773700ris, Allen E.
ON NUMBER: 34,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELECOMMUNICATION INFORMATION TELEPHONE: (415) 354-3592
                                                                                                            TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4970 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-1993
                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-MAI APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                    ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-764-100-20/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 TATTTTTATATATAGTTTGCTTATTTAACACTTATTTAGACAAATTAAATTTATTGATTA 415
                                                                                                                                                                                                                                                                                                                          Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Goldbach, Robert W.
TITLE OF INVENTION: Improvements in or Relating to Organic
TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                        Score 50.2; DB 2; Length 4
Pred. No. 0.089;
0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALT: 343.04
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 aaagcattcatcatttaatacattaaaaaatattt 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van Grinsven J., Martinus Q.
De Haan, Petrus T.
Gielen L., Johannes J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/764,100 FILING DATE: 06-DEC-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 08/032,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: GB 9206016.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08764100 Patent No. 5773700
        ATTORNEY AGENT INFORMATION:
NAME: No. 5773700ris, Allen E.
REGISTRATION NUMBER: 34,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sandoz Agro, Inc
975 California Avenue
                                                                  REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
                                                                                                        TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
INFORMATION FOR SEO ID NO: 16
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            3.8%;
FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-MAR-1993
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                                                                                                                                                                                     LENGTH: 473 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                        Query Match 3.8
Best Local Similarity 52.1
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peters, Dirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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US-08-764-100-16
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APPLICANT:
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3738 AAAACCAAAAAATTTTTTTTTTTAAATAAATAAGCCTCCGGCCAGATTTGGTCTAAGACC 3679
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                                                                                                                                                                                                                                                                                                                        Length 4970;
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Pred. No. 0.12;
0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 aaagcattcatcatttaatacattaaaaaatattt 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence enc
TITLE OF INVENTION: phosphate synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSTEM: PC-DOS/MS-DOS
Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08446855A Patent No. 5849573
                                     5773700ris, Allen E.
                                                       REFERENCE/DOCKET NUMBER: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart, Thomas S
Flores, Maria V
                                                                                            ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.00
                                                                                                                                                                                                                                                                                                                      Query Match 3.8%;
Best Local Similarity 52.1%;
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTORNEY/AGENT INFORMATION:
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                                                                                                                              TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     4970 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arlington
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                                                                                                                                                                                                                           STRANDEDNESS:
FILING DATE:
                                                                                                                TELEPHONE:
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US-08-764-100-20
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                                                                                                                                                                                         LENGTH:
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8671 ATGTATAAACCAAAATGGTTTTTTCAATTTACAAATAATTTTATAATTTTAATAATTTA 8730
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                                                                                                                                Score 50.2; DB 3; Length 8920;
Pred. No. 0.13;
0; Mismatches 123; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abortive Infection Protein
From Lactococcus
lactis, and Method of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Holler, Peter A. Vandenbergh,
Ebenezer R. Vedamuthu, Jeffrey K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA Encoding Phage TITLE OF INVENTION: Abortive Infection TITLE OF INVENTION: From Lactococcus TITLE OF INVENTION: lactis, and Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS (version SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sylvain Moineau, Barbara
J. Holler, Peter A. Vande
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08565907A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8731 TTAATTATAAAAAAAAA 8749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 tttaatactaacagtagag 300
                                                                                                                                    Query Match 3.8%;
Best Local Similarity 52.1%;
Matches, 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                  STRANDEDNESS: single
                                                       genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Okemos
STATE: Michigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acer
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                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                          US-08-446-855A-1
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us-09-464-528-6.rni

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NAME/KEY: phage abortive infection LOCATION: N/A LOCATION: N/A LOCATION METHOD: sequencing orner information: DNA encoding phage OTHER INFORMATION: resistance
TELERAX: (517) 347-4100
TELEX: (517) 347-4103
TELEX: No. 58144999
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 4467
                                                                                                                                                                                                                                                           ORGANISM: Lactococcus lactis
                                                                                                                                                                               Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUBLICATION INFORMATION:
US-08-565-907A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: SMQ-20
OSITION IN GENOME: N/A
                                                                                                                         STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE: N/A
SELL TYPE: bacterium
SELL LINE: N/A
                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                      MMEDIATE SOURCE:
LIBRARY: genomic
                                                                                                                                                                                                                        FRAGMENT TYPE: N/A
                                                                                                              Nucleotide
                                                                                                                                                                                            Ñ
                                                                                                                                                                                                             ANTI-SENSE: NO
                                                                                                                                             TOPOLOGY: L1
                                                                                                                                                                                                                                                                                                                                                       CELL TYPE:
CELL LINE:
ORGANELLE:
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2679 ATTIAAATCAATIAAGTITAGTAATTCTTCTTGATTAATAAATCATCTATTTCAAAGAC 2620 2619 AACCATATACAACAATATTGATATAATTCTTGATTAAAATTATTTTACGATAGTGGTC 2560 111 aaagattttttaaaaaaatgtataaaattattattoatgattttcatacatttgatt 170 171 tigataajaaatatattittittaatticitaaaaaaaqitigcaagacacttattagaca 230 Query Match 3.8%; Score 49.8; DB 2; Length 4467; Best Local Similarity 49.4%; Pred. No. 0.14; Matches 129; Conservative 0; Mismatches 132; Indels 0; a

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Search completed: September 2, 2000, 01:57:31 Job time: 8215 sec

1 tctagatcaaactcacatcc.....tttttgaagtataaccatgg 1314 311585 seqs, 125096042 residues IDENTITY_NUC Gapext 1.0 Scoring table: Sequence: Searched:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

																															•				
		Description			x virus b	sedneuce	cDNA encoding Plas	Plasmodium berghei	Sequence encoding	Plasmodium var-7 g.	3	Plasmodium var-7 g	Borrelia burgdorfe	Human 3' apolipopr			Orpinomyces cellul	pNPX30 xylanase cD	Carbamoyl-phosphat	Human 3' apolipopr	Malaria-specific g	SERP gene. Recombi	Sequence encoding	Borrelia burgdorfe	cDNA encoding Plas	_		Sequence of ANS-1	Pythium oligandrum	Pythium oligandrum	MS-Le1610 Vector.	i mn i			Impatiens Necrotic
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SUMMARIES		;																						•									11		
SUMM		O.	X33181	X33182	X33180	X33184	T41852	V33135	N60472	T72882	V29580	T72882	X20251	T31530	X20253	V37413	V29477	053480	062924	T31530	N81157	022999	003568	X20253	T41852	X20361	V33136	N71405	V29578	V29578	055185	T58577	V21209_	9	049959
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•	Query	Match	5.0	٠	5.0	٥.			4.3	4.3	4.1	4.1	4.0	4.0	4.0	4.0	4.0	4.0	4.0	3.9	3.9	3.9	3.9	٠.	٠.	3.9	•		٠.	•	6 6	3.9	3.9	3	3.8
		Score	'n.	65.8	ď.	ď.	6	ė.	26	26	54.2	53.6	53.2	. 52.6	52.4	52.2	52.2	52.2	52	51.8	51.8	51.8	51.8	51.8	51.4	51.2	51.2	51.2	51.2	51.2	51	6		50.2	50.2
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Sequence encoding Carbamoyl-phosphat	Sequence encoding pSRQ800 fragment i	Thymidylate phosph Borrelia burgdorfe	Tox2a gene. DNA en	portion xylandse cu 50 kD subunit of S	Medium chain-speci P. falciparum live	Continuation (13 o
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Q03568 Q62924	Q25273 T68648	Q12528 X20251	024177	Q24134	T43682 T78867	V21209_12
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34	36 37	38	0 7	4 4 1 7	443	45
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ALIGNMENTS

RESULT

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n	
AC	, X33181;
Z	25-JUN-1999
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X	Cowpox virus;
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PD	18-MAR-1999.
PF	07-SEP-1998;
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႘	The present invention describes an apoptosis-resistant virus-sensitive
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ပ္ပ	obtain a recombinant virus naving the integrated apoptosis associated
8 8	gene. In this invention an apoptosis-resistant 293 cell
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New apopucasis issistance...

Example 2: Page 41-45: 51pp; English.

The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction autoimmune diseases. Prior arts have
                                                                  ttagcgaattttgtaattgtacttgtttgtctgtagttttgttttgttttcttgtttctc 1058
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                                                                                                                                                                                                                                                                                  aatcatttcataattgcctttctttctttagcttatgagaaataaaatcattttttt
tgcacttctggtttgctttgccttgcttttcctcaactgggtccatctaggatccatgt
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WO9913073-A2.
18-WAR-1999
07-SEP-1997; JP-259235.
(RPRG-) RPR GENCELL ASIA PACIFIC INC.
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encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cell. the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having a problem. The present sequence represents the base sequence of the plasmid pRx-Bc1-X1-bsr, which contains the human Bc1-x1 gene, and is used in an example from the present invention.

Sequence 7372 BP: 2353 A; 1749 C; 1649 G; 1621 T;
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                                                                                                                                                                                                                             Length 7372;
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                                                                                                                                                                                                                             Score 65.8; DB 1;
Pred. No. 0.0045;
0; Mismatches 372;
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X33180/c
ID X33180;
AC X33180;
DT 25-JUN-1999 (first entry)
DE Cowpox virus bsr full length gene sequence.
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Best Local Similarity 43.7%;
Matches 289; Conservative
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which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the cowpox virus bsr gene which
                                                                                                                                                                                                                                                                                                                                                             The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              obtain a recombinant virus having the integrated apoptosis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     required to replicate and produce the virus, resulting in failure to
Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autolmmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1656 G;
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                                                                                                                                                                                                                                                                                                                  New apoptosis-resistant virus-sensitive cell
                                                                                                                                                                              07-SEP-1998; J04010.
08-SEP-1997; JP-259235.
(RPRG-) RPR GENCELL ASIA PACIFIC INC.
                                                                                                                                                                                                                                                                                                                                          Example 1; Page 34-38; 51pp;
                                                                                inflammatory disease; ss
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                                                                                         939 atttcaaaataaaccttgggccttgtgctgactgagatggggtttggtgattacagaatt 998
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 DB 1; Length 7797;
Query Match
5.0%; Score 65.8; DB 1; Length 7
Best Local Similarity 43.7%; Pred. No. 0.0045;
Matches 289; Conservative 0; Mismatches 372; Indels
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	ò	1299 t 1299
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	RESULT X33184	LT 4 847c
	A	X33184 standard; DNA; 7996 BP.
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	XW	id pRx-Bcl 2-i-hCD 25. ector: expression; apobtosis;
-	X	bcl-x1; FLI
	X X	sease; grait rejection reaction; init disease; ss.
	SO	
	os N	Homo sapiens. W09913073-A2.
	B	18-MAR-1999.
٠.	PF	J04010.
	PA	(RPRG-) RPR GENCELL ASIA PACIFIC INC.
		Hamada H;
		WFI; 99-243/20/20. New apoptosis-resistant virus-sensitive cell
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	ខ្លួ	The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance qene has been introduced.
	႘	The recombinant viruses generated are capable of expressing apoptosis-
,	ဗ္ဗဗ္ဗ	딕걸
	ខ	inhibition of harmful apoptosis; is therapeutic. The recombinant viruses
	ე წ	are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of
	ខូ	autoimmune diseases and graft rejection reaction, and apoptosis induction
	ពួម	therapy for inflammatory cells in inflammatory diseases. Prior arts have
	ខ	expressing an apoptosis-associated gene is introduced into animal cells,
	ပ္ပင္ပ	the cells producing the virus will be destroyed because the period of
	88	required to replicate and produce the virus, resulting in failure to
	ပ္ပင္	obtain a recombinant virus having the integrated apoptosis-associated
	38	apoptosis resistant gene introduced) is established and overcomes the
	႘	oblem. The present sequence represents the base sequence of the
	ខ្លួ	21 2-1-nCD 25, which contains the number 2 gene, a example from the present invention.
	SO	quence 7996 BP; 2463 A; 2015 C;
	õ	5.0%; Score 65
	W P	best Local Similarity 43.7%; Fred. No. 0.0042; Matches 289; Conservative 0; Mismatches 372; Indels 0; Gaps
	δy	639 agttgagaccaagacacactcgttcatatatctctctgctcttctcttcttctacctc 698
	q	5794 AGCTICGACCAATICTITITITITITITITITITITITITITITITI
	δy	699 tcaaggtacttttctccctctaccaaatcctagattccgtggttcaatttcggatct 758

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818 5615	878 5555	938 5495	998 5435	1058 5375	1118	1178 5255	1238 5195	1298											· ~		
Oy 759 tgcactctggtttgctttgcttttcctcaactgggtccatctaggatccatgt 	Oy 819 gaaactctactttctttaatatctgcggaatacgcgttggacttcagatctagtcga Db 5614 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Oy 879 aatcatttcataattgcctttctttttagcttatgagaaataaaatcatttttttt	y 939 atticaaaaaaccttgggccttgtgctgagatggggtttggtgattacagaatt	y 999 ttagcgaatttcgtaattgtacttgtttgtctgtagttttgttttgtttcttgtttctc	y 1059 atacattccttaggcttcaattttattcgagtataggtcacaataggaattcaaactttg	Oy 1119 agcagggaattaatccttccttcaaatccagtttgtttgt	Oy 1179 aaacttttgctttaaattctattataacttttttatggcaaaatttttgcatgttct 	y 1239 ttgctctcctgttgtaaatttactgtttaggtactaactctaggcttgttgtgcagtttt	y 1299 t 1299	b 5134 T 5134	RESULT 5	741852 standard; DNA; 9789 BP.		Plasi Key cds	/*tag= /product misc_feature 518.52	/*tag= /transl_ misc_feature 656. 65	/ _ray= c // _ray= c // Transl_except= ATT encodes Leucine // ransl_except= ATT encodes Leucine // ray= 2911 // ray= d // ray= d	/transl_ misc_feature 34613	/transl_ misc_feature 55465	/transl_ misc_feature 62546	FT /*tag= g /transl_except= AAT encodes Lysine
φ Δ	ç g	0 0	9 9	65 G	o d	강 원	\$ 8	o G	ò	පි	E E	102	X X D D T	O # #	[14 [14 [14]	أساك متامداً	ւնւնւն	عابدا بدا	عا بنا بنا .	, (24, (24, (14 E4

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116 ttttttaaaaaaatgtataaaattatattcatgattttcatacatttgattttgat 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A polypeptide comprising a plasmodium falciparum (Pf) erythrocyte membrane protein 1 (PfEMP1) or active fragments or analoques of that protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMP1 gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primers used to generate characteristic amplification patterns from different P. falciparum strains, Antibodies specifically immunoreactive with the PfEMP1 polypetide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the PfEMP1 protein of the MC type of Plasmodium falciparum. An alternative, truncated version of the coding sequence (a cDNA clone) is given in T41853.

4061 A; 1393 C; 1837 G; 2498 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Plasmodium falciparum erythrocyte membrane proteins - used to develop products for the diagnosis, treatment or prevention of malaria parasite infections
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                                                                                                                                                                                                                                                                                                                                                       /transl_except= ATT encodes Asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_except= GGA encodes Tryptophan 7754. .8478
                                                                                                                                                                                                   TTC encodes Isoleucine
                                                                                                                                                                                                                                                                             _except- ATA encodes Histidine
                                                  ATA encodes Tyrosine
                                                                                                                         _except= AAC encodes Lysine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1996; U05798.
27-APR-1995; US-430908.
(APRY-) AFFYMAX TECHNOLOGIES NV.
BATUCH DI, HOWARD RJ, PASIGSKE BL;
WPI; 96-497376/49.
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tagaatcttcttgtgagtggtgtgggagtaggcaacctggcattgaaacgagaaagag 355

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Detecting Plasmodium. Infection from hybridisation with extrachromosomal element - providing genus or species specific diagnosis with few false negatives, in humans or animals or claim 15: Page 54-59; 120pp; English.

Claim 15: Page 54-59; 120pp; English.

Claim 15: Page 54-59; 120pp; English.

This is the nucleotide sequence of one strand of the PSI-PL470 gene of the 30.7 kb extrachromosomal plastid of Plasmodium berghei.

This plastid encodes organelle-like rRNAs, tRNAs, ribosomal proteins and RNA polymerase subunits, amongst others. Plasmodium is detected in a human or animal sample by treating it, or derived nucleic acid, with a Plasmodium extrachromosomal genetic element or derived nucleic acid (A) and detecting any hybridisation. (A) can include the PSI-PL470, PLH-PPH, PRB or PWO gene, the mitochondrial coxI gene, and nucleic acids derived from them. Also new are considered probes and primers (see v33139-56). The method is polypeptides encoded by (A) are useful as targets for drug development and for development of anti-malaria vaccines. The high development and for development of anti-malaria vaccines. The high development of genus- or species-specific assays that result in fewer false negatives than known methods (typically 1% against 3%). Sequence 5849 BP; 2296 A; 673 C; 2323 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 ttttcatacatttgattttgataataaatatatttttttaattcttaaaaaatgttgc 213
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Query Match
4.3%; Score 56.4; DB 1; Length 5849;
Best Local Similarity 53.1%; Pred. No. 0.15;
Matches 120; Conservative 0; Mismatches 106; Indels 0
                                                                                                                                                                                                                                                                                                                                                07-DEC-1998 (first entry)
Plasmodium berghei plastid PSI-PL470 gene.
Malaria: infection; therapy; diagnosis; vaccine; plastid;
PSI-PL470 gene; ds.
Plasmodium berghei ANKA strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 aagacacttattagacatagtcttgttctgtttacaaaagcattca 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kara AKU, Nelson JS, Tan TMC, Tham JM, Ting RCY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-FEB-1997; AU-004953.
21-APR-1997; AU-006352.
(MOLE-) INST MOLECULAR 6. CELL BIOLOGY.
(UYSI-) UNIV SINGAPORE NAT.
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N60472;
24-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                   V33135 standard; DNA; 5849 BP
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DBL gene family; SABP; sialic acid binding protein; vaccine; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (N60472) or FIRA (N60473). RESA and FIRA have antigenicity suitable for providing protective immunity against Plasmodium falciparum malarial infections. Sequence 4590 BP: 1933 A; 437 C; 673 G; 1547 T;
Sequence encoding the ring-infected Erythrocyte Surface Antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA coding for Plasmodium falciparum antigens - expressing poly:peptide(s) having antigenicity of RESA or FIRA antigens falciparum
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WPI; 86-094065/14.
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DABP; merozoite; malaria; var-1; var-2; var-3; var-7; in
                                                                  antigen; epitope; ss.
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Plasmodium vivax.
Plasmodium falciparum.
Location/Qualifiers
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(HALL-) HALL INST MED RES.
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                                                                                                   plasmodium falciparum
                                                        Malaria vaccine;
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Martin FN;
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                                                                                                                                                                                                                        claim 4; Page 56-61; 96pp; English.

This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and sialic acid binding protein (DABP) and sialic acid binding protein (SABP) conserved regions (see 772889 and 772888 respectively). The var family of genes modulate cytoadherence and antigenic variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture superantant after infected erythrocytes release merosofies. DABP and SABP mediate the binding of merosofies and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention. The compositions are necessary for erythrocyte invasion by the parasite and colectide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective lammal to plasmodium merozoites (especially Plasmodium and Plasmodium merozoites (especially Plasmodium and Plasmodium merozoites (especially Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1444 TTAGTATTTTAATAATAAATAAATCTTTTAAAAAACTTCAAAACATTTTTGCATAAAATA 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 ataaatatatttttttaatttcttaaaaaatgttgcaagacacttattagacatagtct 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgttctgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatactaacagt 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 agaatettettgtgagtggtgtgggagtaggcaaeettggeattgaaaecgagagaaagaga 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-5EP-1998 (first entry)
Pythium oligandrum isolate 23-5 mitochondrial DNA partial sequence.
Pythium oligandrum; phytopathogenic; mitochondrial DNA; fungus;
                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                New malaria vaccines - contains cysteine-rich DBL fupily proteir binding domains homologous domains of the Duffy and stalic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 1; Length 19124;
Pred. No. 0.17;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1564 ATTAGAACAAAAAGAATATTACAAAAAATAATAAAATTAAATTA 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Su X;
                                                                             07-JUN-1995; US-487826.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Chitnis C, Miller LH, Peterson DS, Sim KL,
               /note= "no stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 164; Conservative
 /number=
                                                              07-JUN-1996; U09508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                              WPI; 97-052231/05.
P-PSDB; W22475.
                                                                                                                                                                                                                   proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                 Wellems
                                                                                                                                                                                                                 binding
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V29580/c
ID V2958
AC V2958
DT 04-SE
DE PYTHI
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Claim 17; Page 30; 41pp; English.

This is a partial nucleotide sequence of the mitochondrial DNA from a pythium oligandrum isolate 23-5. Nucleotide sequences which are inverted repeats, flanked by Peti restriction sites from mitochondrial DNA from various P. oligandrum isolates are shown in V19576 to V19583. These Pythium isolates are non-pathogenic and can be used in a method for controlling phytopathogenic organisms where the organisms are contacted with such a Pythium isolate. The Pythium isolates are used to contacted with such a Pythium isolate. The Pythium isolates are used to contact ingi. Specifically pathogenic Pythium solates are used to other soil borne pathogens), particularly for protecting plants (seedlings, transplants or vegetable crops such as tomato) against isolate sequences are useful as sources of probes for identification of particular isolates. The isolates are widely distributed in nature, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a similar ecology to pathogenic species. They produce large quantities of cospore inoculum on liquid or solid substrates and are tolerant of several commonly used fungicides. A single application at the greenhouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmodium var-7 gene.

DBL gene family; SABP; stalic acid binding protein; vaccine; therapy;
Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 TTATTAGAAGTATTTTCATTTTAATTTTTTTTAAAAGTTATATATTTTAAAAAGATAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 TATTGAAGAATTTCTTATAACTACTATTAAAGATTTATAGGATCTACTGTATAAATCCAG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aagattttttaaaaaaatgtataaaattattattcatgatttttcatacatttgattt 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 98-250977/22.
Controlling phytopathogenic organisms with non-pathogenic Pythium
isolate - for control of damping off caused by Pythium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
   pathogen; tomato; mycotoxic; plant protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54.2; DB 1; Length 1186;
Pred. No. 0.33;
0; Mismatches 73; Indels 4
                                                                                                                                                                   /*tag= a
/note= "unique fragment claimed in claim 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stage will protect plants after transplanting Sequence 1186 BP; 469 A; 121 C; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
7317 .15139
/*tag= a
                                                                                                   Location/Qualifiers
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                                                                                                                              502. .684
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Best Local Similarity 59.3
Matches 112; Conservative
                                                                                                                                                                                                                                                                                           7; U18343.
5; US-731722.
                                                                                                                                                                                                                                                         23-APR-1998.
10-OCT-1997; U18343.
17-OCT-1996; US-731722
(UYFL.) UNIV FLORIDA.
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Plasmodium falciparum.
soil saprophyte; pat
vegetable crop; ss.
Pythium oligandrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 agtcttgtt 240
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                                                                                                                              misc_feature
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T31530 standard; cDNA; 605
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T31530
ID T31530
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                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 56-61; 96pp; English.

Claim 4; Page 56-61; 96pp; English.

This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to the Duffy anning protein (Dame) of genes which have homology to the Duffy anningen binding protein (Dame) as a fact of binding protein (Dame) and T7288 respectively). The var family of genes modulate cytoadherence and antigenic variation of Family of genes modulate cytoadherence and antigenic variation of protein (DABP) are soluble proteins that appear in the culture cyportein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP comediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and comprise either a nucleotide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to Plasmodium merozoites (especially Plasmodium falciparum or Plasmodium vivax).

Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1058 catacattccttaggcttcaattttattcgagtataggtcacaataggaattcaaacttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New malaria vaccines - contains cysteine-rich DBL family protein
binding domains homologous domains of the Duffy and sialic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.1%; Score 53.6; DB 1; Length 19124;
45.9%; Pred. No. 0.41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259;
                                                                                                                                                                       19-DEC-1996.
07-JUN-1996; U09508.
07-JUN-1995; US-487826.
07-JUN-1995; US-487826.
Chitnis C, Miller LH, Peterson DS, SIM KL,
                                                                                                                 /number= 2
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
   /number= 1
15140. .16205
                                                           /number= 1
16206. .17552
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Matches 221; Conservative
                                        *tag=
                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                      WPI; 97-052231/05.
                                                                                                                                                                                                                                                                                                                                                               binding proteins
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33384 AAATATTAAATATTAAATATTAAATATTTTAAAACAATTAAAATTTTTATATTAAAAATG 33325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in humans and Borrelia causes epidemic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 aaacataacatggatatctccttaccaatcatactaattattttgggttaaatattaatc 80
                                                                                                                                                                                                                                                                                                                                                                                           Borrella burgdorferi polynucleotide sequence #4.
Borrella burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borrellosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 53585;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 taaaaaatgttgcaagacacttattagacatagtcttgttctgttt 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7001 G;
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Pred. No. 0.48;
0; Mismatches 108;
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                                                                                                                                                                                                                                                                                     K20251/c
ID X20251 standard; DNA; 53585 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN GENOME SCI INC.
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Matches 118; Conserv
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                                                                                                                                                                      15462 TT 15461
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                                                                                                              1298 tt 1299
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193 taatttottaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaa 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi polynucleotide sequence #6.
Borrelia burgdorferi: spirochete; bacterium; pathogen; Lyme disease;
epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   claim 7; Rage 59-60; 84pp; English.

Human apoliopprotein B (apoB) scaffold attachment region (SAR)
element clones Rh32 (731530) and Rh10 (731531) respectively carry
the 3' human apoB SAR element and the distal 1212 bp 5' human apoB
SAR element and 1317 bp proximal sequence. These SAR elements
co-map with the boundaries of the human apoB gene chromatin
domain. A novel recombinant DNA molecule adapted for transfection
of a host cell comprises an erythropoietin (EPO) cDNA (731529) or
genomic clone (731532) operably linked to an expression control
increase expression of the recombinant EPO in stable, long-term
                                                                                                                                                                                                                                    Recombinant DNA molecule expressing mammalian erythropotetin useful to transform cell lines, and for gene therapy, e.g. of anaemia and other red blood cell disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%; Score 52.6; DB 1; Length 605; 55.1%; Pred. No. 0.6;
                                                Erythropoletin; EPO; anaemia; gene therapy; vector;
scaffold attachment region; SAR element; apolipoprotein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R, Dougherty BA, Fraser C, Lathigra R, Smith
                                 SAR element clone Rh32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X20253 standard; DNA; 26811 BP.
                            duman 3' apolipoprotein B SAR
Irythropoletin; EPO; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 A;
                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 55.1
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammalian cell cultures.
                                                                                                                                                            19-DEC-1994; US-358918.
(CANG-) CANGENE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1998; U12764.
03-SEP-1997; US-057483
20-JUN-1997; US-050359
22-JUL-1997; US-053344.
                                                                                transgenic animal; ss
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                                                                                                                                              8-DEC-1995; CA0696
                                                                                                                                                                                                                  WPI; 96-309587/31
T31530;
15-SEP-1996
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DD 14828 TAAATTAATTGAATTTTAAAAATTAGAATTAAAATTCTAAATTTCATATTAA 14887
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White OR;
WPI: 99-081217/07.
WPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tor, e.g. producing recombinant Orphingres cellulase process of the form of the form of the following recombinant Orphingres cellulase in host cellulations of the following recombinant Orphingres cellulase in host cellulations of the anacrobic bovine rumen fungus Orphingres sp. pc-2. It was obtained by screening a pc-2 cDNA library for clones active on remazol brilliant blue-cerboxymethylcellulase. The encoded cellulase has endoglucanase, but not celloblohydrolase, activity. CelA and celC genes (see V29472-73), also obtained from Orphingres sp. pc-2, encode cellulases having both activities (see W56738-39). Recombinant DNA molecules encoding Orphingres cellulase proteins are claimed, as well as recombinant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA encoding Orpinomyces cellulase protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 cttaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattc
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Aspergillus, Trichoderma reesei, Pichia, Penicillium, Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%; Score 52.4; OB 1; Length 26811; 52.3%; Pred. No. 0.64; Live 0; Mismatches 106; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3596 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 14948 TAAAGAGTTTAAAAACTTTCTTATATATTTCTAACAAAAGCA 14989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 atcatttaatacattaaaaaatatttaatactaacagtagaa 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orpinomyces cellulase CelB cDNA.
Cellulase; endoglucanase; CelB gene;
Orpinomyces sp. strain PC.2.
Key.
Location/Qualifiers
CBS 69.1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V37413 standard; cDNA to mRNA; 1826
V37413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
69. 1484
/*tag= a
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04-0CT-1996; US-0Z7883.
(UYGE) UNIV GEORGIA RES FOUND INC.
Chen H. Li X. Liungdahl LG;
WPI; 98-240096/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8978 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.0
Best Local Similarity 52.3
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26811 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                      193 taatttotttaaaaaatgttgcaagacacttattagacatagtttgttotgtttacaaaa 252
                                                                                                                      Gaps
                                                                                                                                                     toacatcoaaacataacatggatatctccttaccaatcatactaattattttgggttaaa 72
or Bacillus, and a method for producing recombinant cellulase by culturing these host cells.
Sequence 1826 BP; 654 A; 236 C; 313 G; 623 T;
                                                                                     Length 1826;
                                                                                   Score 52.2; DB 1; Length 1
Pred. No. 0.69;
0; Mismatches, 133; Indels
                                                                                   49.88;
                                                                                 Query Match
Best Local Similarity 49.8
Matches 132; Conservative
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New recombinant DNA encoding Orpinomyces cellulase protein useful for, e.g. producing recombinant Orpinomyces cellulase in host cell for, e.g. producing recombinant Orpinomyces cellulase in host cell This cDNA clone includes a claimed coding region for cellulase celB (see w56742) of the anaerobic bovine rumen fungus Orpinomyces sp. 67-2. It was obtained by screening a PC-2 cDNA library for clones active on remazol brilliant blue-carboxymethylcellulose. The encoded cellulase, has endoglucanase, but not cellobiohydrolase, orthing and celC genes (see V29472-73), also obtained from Orpinomyces sp. PC-2, encode cellulases having both activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (see W56738-39). Recombinant DNA molecules encoding Orpinomyces cellulase proteins are claimed, as well as recombinant cells selected from Saccharomyces cerevisiae, Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus, Trichoderma reesel, Pichia, Penicillium, Streptomyc
or Bacillus, and a method for producing recombinant cellulase by
                                                             21-SEP-1998 (first entry)
Orphiomyces cellulase Cells CDNA.
Cellulase; endoglucanase; CelB gene; ds.
Orphiomyces sp. strain PC-2.
                                             V29477 standard; cDNA to mRNA; 1826 BP
                                                                                                                                                                                                  Location/Qualifiers.
69. .1484
                                                                                                                                                                                                                                                                                                                                                       03-OCT-1997; U18008.
04-OCT-1996; US-027883.
04CT- UNIV GEORGIA RES FOUND INC.
Chen H, L1 X, Ljungdahl LG;
MPI; 98-240096/21
                                                                                                                                                                                                                                                       /*tag= a
/note= "Claim 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            culturing these host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orpinomyces sp. PC-2
(see W56738-39). Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; W56742
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RESULT
V29477
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Gaps

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4.0%; Score 52.2; DB 1; Length 1826; 49.8%; Pred: No. 0.69; iive 0; Mismatches 133; Indels 0;

Query Match
Best Local Similarity 49.8
Matches 132; Conservative

Streptomyces

· 623 T;

313 G;

236 C;

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1681 AAAAAGTTTAATAAATGATAAAAAAAATATTAAACATTTTGGATGTATTTGCATATCAA 1740
                                                193 taatttottaaaaaatgttgoaagacacttattagacatagtottgttctgtttacaaaa 252
13 tcacatccaaacataacatggatatctccttaccaatcatactaattattttgggttaaa 72
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2, 2000, 01:56:29 Search completed: September Job time: 8558 sec

1681. AAAAAGTTTAATAATGATAAAAAAAATATTAAACATTTTGGATGTATTTGCATATCAA 1740

253 gcattcatcatttaatacattaaaa 277

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AL021939 Homo sapi
AC001512 Homo sapi
AC005504 Plasmodiu
AC008576 Homo sapi
AC026640 Homo sapi
AC026640 Homo sapi
AC02331 Homo sapi
AC02331 Homo sapi
AC05505 Plasmodiu
U87514 Dictyosteli
AC06278 Plasmodiu
X0465 Marchartia
AL142826 Anopheles
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AL139177 Homo sapi
AL034419 Human DNA
AJ223323 Saccharom
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ACO06095 Homo sapi
ACO09653 Homo sapi
ALO49180 Plasmodiu
ACO18919 Homo sapi
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PFMAL13P1
AC018919
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Match Length DB
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                                                                                             September 1, 2000, 23:32:16; Search time 5217.98 Seconds (without alignments) 449.425 Million cell updates/sec
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1314
1 tctagatcamactcacatcc......tttttgamgtatamaccatgg 1314
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 1000000
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qb_ba2:
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Perfect score:
Sequence:
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166494 Sequence 14

Description

Z to Z	JOURNAL SUBMILTED (10'MAY-1998) sanger ac. uk/HGP/Chrb/) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquires: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk COMMENT On May 18, 1998 this sequence version replaced g1:2009620. IMPORTANT: This sequence is the entire insert of clone 352A20. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of hunan chromosome 6, constructed by the Sanger Centre chromosome 6 hunan chromosome 6, constructed by the Sanger centre chromosome 6 hute; //www.sanger.ac.uk/HGP/Chr6/ This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated hunan repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 352A20 is at 1 in this sequence. The true right end of clone 352A20 is at 1 in this Saguence. The true left end of clone 352A20 is at 144759. 352A20 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.	FEATURES Location/Qualifiers 1. 144759 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Rp3-352A20" /clone="Rp3-352A20" /clone="Rp3-352A20" /clone="lib="RPCI-3" 3211 /note="AluSc repeat: matches 77285 of consensus: incomplete repeat: matches 462 of consensus: note="AluSc repeat: matches 1299 of consensus" /note="Musc repeat: matches 1299 of consensus" repeat_region /note="AluSc repeat: matches 640811 of consensus" repeat_region /note="LipB3 repeat: matches 640811 of consensus" /note="LipB3 repeat: matches 2991 of consensus" /note="AluSc repeat: matches 2991 of consensus" /note="AluSc repeat: matches 9411046 of consensus" /note="LibM4A repeat: matches 9411046 of consensus" /note="LibM4A repeat: matches 9411046 of consensus"
AC006269 Homo sapi AC009277 Homo sapi M33862 Dictyostell AL031746 Plasmodiu AC01108 Mus muscu AC01008 Mus muscu AC01008 Two yeast m J01533 Yeast (S.ce AC031982 Homo sapi AC031982 Homo sapi AC031981 D. teissieri AC01373 Homo sapi AC01373 Homo sapi AC01375 Homo sapi AC01375 Homo sapi AC01077 Homo sapi AC01077 Homo sapi AC01077 Homo sapi AC010772 Homo sapi AC010772 Homo sapi AC010772 Homo sapi AC010772 Homo sapi	1367. PAT 28-DEC-1997 Falkner, F. Gunter. 1997; 929 t 368 others DB 5; Length 7218; 0.072; ches 136; Indels 0; Gaps 0;	ttocctataaattggaactcaatgct 613 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
25 66.2 5.0 167271 53 ACC06269 26 66.2 5.0 226345 39 ACC062406 28 65.8 5.0 226345 39 DDISGSPA 29 65.8 5.0 68746 43 ACC0108 31 65.8 5.0 68746 43 ACC2108 32 65.4 5.0 68746 43 ACC2108 33 65.4 5.0 6877 41 ACC04086 34 65.2 5.0 161891 52 ACC08206 35 65.2 5.0 161891 53 ACC01349 36 65.2 5.0 287731 59 ACC01352 37 65.2 5.0 287731 59 ACC01352 38 65.4 9 6912 43 ACC1351 39 65.8 4.9 6912 43 ACC1351 44 64.8 4.9 173693 57 ACC1352 45 64.6 4.9 52359 41 ACC10772 46 44 4.9 173693 73 ACC1622 46 64.4 4.9 22359 41 ACC10772 46 64.4 4.9 217442 73 ACC1622 45 64.2 4.9 15367 57 ACC11212	SULT 1 6494 CUS CUS CESSION RESION RESION TWOEDS ORGANISH ORGANISH AUTHORS TITLE AUTHORS AUTHORS SE COUNT IGIN	Oy 554 cttttccgtcattaactcaccctgccacccggtttccctataaattggaactcaatgct

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OR1 repeat: matches 139. .236 of consensus"
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                                                                                                                                                        104 of consensus;
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complete repeat"
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                                                                                                    note-"AluSq repeat: matches 303. .1 of consensus"
224. .8333
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19. .11210
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29632
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32032
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.34079
                                                                     .146 of consensus"
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14497
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12. .11507
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52. .15077
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         .301
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lote-"AluY repeat: matches 300.
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16. .31711
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5475
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24456
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note="AluJb repeat: matches 3.
863, .4153
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                                                                     MIR2 repeat: matches 80.
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ote-"L1PA13 repeat: matches 896. .463 of consensus
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te="MER21A repeat: matches 568. .11 of consensus"
08. .49633
te="MER1B repeat: matches 332. .1 of consensus"
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7780. .58075
7780. s8075
8145. .58288
note="AluSp repeat: matches 302. .157 of consensus."
note="AluSp repeat: matches 302. .157 of consensus."
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                                                                                                                                                                                                                                                                                                                                                                                        ote-"AluJo repeat: matches 133. .64 of consensus;
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46980
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                                                                          1027. .39331
note="AluSq repeat: matches 303. .1 of consensus"
2819. .43105
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.ncomplete repeat"
                                                    ote-"AluJo repeat: matches 302, .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                          MIR2 repeat: matches 2. .145 of consensus" .47547
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Pred. No. 0.098;
0; Mismatches 105; Indels 1;
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16. .49238
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                                                                                                           1819. .43105
note="aluSx repeat: matches 1. .299 of
1829. .43567
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44043
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te="match: STS G13944"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 12, 2000 this sequence version replaced 91:6139137. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 153267)
Db 113389 TTTTATATATATATATATTTTTT-ATATATTTTTTTTATATATATATATATATTTTT 113447
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                                                                                                                                                                                                           228 acatagtettgttetgtttacaaaageatteateattaatacattaaaaaatatttaat
                                                                                            168 attttgataataaatatattttttttaatttcttaaaaaaatgttgcaagacacttattag
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Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 111839 bases at least 040 Consensus quality: 133540 bases at least 030 Consensus quality: 144810 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               irren, B., Linton, L., Nusbaum, C. and Lander, E. Duo sapiens, clone RP11-3N16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; M77815; 100% of
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 12897 bp in length
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contig of 10109 bp in length
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contig of 4492 bp. in length
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contig of 4288 bp in length
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contig of 6838 bp in length
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contig of 3368 bp
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'note-"assembly_fragment"
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'note="assembly_fragment"
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4806. .7966
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'note="assembly_fragment'
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15687. .19054
a 'working draft'
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134718: conti
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4705: co
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7966: cor
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10438: co
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1353 2550: c
2551 2650: gap o
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Kurdi, O.B., Conway, A.B.
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Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Tamaki,T., Kurdi,O.B.,
Conway,A.B. and Davis,R.W.
                                                                                                                                   Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 aagattttttaaaaaaatgtataaaattatattattcatgatttttcatacatttgattt 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING PROGRESS ***, 3 unordered pieces.
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* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                       yman,R.W., Oin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
irect Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70; DB 41; Length 104992;
Pred. No. 0.35;
); Mismatches 110; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        405 others
                                                                                                                                                                                                                                                                                                                                                                                    58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
04992: contig of 13781 bp in length
                                                                                                                                                                                                                                                                                                                                              contig of 58642 bp in length
gap of unknown lane.
             lyman,R.W., Fung,E.L., Qin,F., Tamaki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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                                                     Lasmodium falciparum 3D7 chromosome
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malaria parasite P. falciparum.
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Best Local Similarity
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="assembly_fragment" 37055 c 36211 g 39185
                                                                                         28135. .31029
/note="assembly_fragment"
31130. 36025
/note="assembly_fragment"
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note-"assembly_fragment"
.00824. .115535
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Consensus quality: 269737 bases at least Q40
Consensus quality: 300872 bases at least Q30
Consensus quality: 310887 bases at least Q30
Consensus quality: 31585 bases at least Q30
Estimated insert size: 349919; sum-of-contigs estimation
Cuality coverage: 1.90x in Q20 bases; agarose-fp estimation
Quality coverage: 1.71x in Q20 bases; sum-of-contigs estimation
                                                           Submitted (03-AUG-1999) Production Sequencing Facility, DO Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94 On Feb 18, 2000 this sequence version replaced 91:6601030.
                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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-----Summary Statistics
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                                                                                                                                                           On Mar 15, 2000 this sequence version replaced g1:6652498 * NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. The true order of the pieces * is not known and their order in this sequence is
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Surren, B., Lintcon, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boudhay, L., Boudhagalter, B., Brown, A., Burtett, G., Cangoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Gint, G., Hagos, B., Heaford, A., Horton, L., Raratas, A., Howland, J.C., Larocque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCkanh, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollyer, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollyer, T., McTerson, R., Peterson, 
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                                                                                                                                                                                                                                                                                                                                                 Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 13, 2000 this sequence version replaced gi:7284664.
                                                                                                                                                                                                                             A HTG 13-APR-2000 clone RP11-69K18 map 11, WORKING DRAFT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164119)
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                                                                                    Gaps
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Length 349919;
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                                                                                Indels
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                                                                            0; Mismatches 107;
                                            0.26;
Score 69.8;
Pred. No. 0.
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SEQUENCE, 16 unordered pieces.
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        Query Match 5.3%;
Best Local Similarity 57.2%;
Matches 147; Conservative
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Genome Center

1188 others

'clone="CTC-557J18" 81094 c 78642 g 92256 t

96739 a

BASE COUNT ORIGIN

/organism-"Homo sapiens

source

FEATURES

/db_xref-"taxon:9606

/chromosome-19

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AC013820 179510 bp DNA HTG 01-APR-2000
Homo sapiens clone RP11-21P24, WORKING DRAFT SEQUENCE, 8 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.35;
0; Mismatches 109;
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note="assembly_fragment"
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/note="assembly_fragment"
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57783. .80005
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Homo sapiens, clone RP11-21P24
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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1 (bases 1 to 1795
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Best Local Similarity 55.3
Matches 135; Conservative
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TITLE
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Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                  Insert size: 176000; agarose-fp
Insert size: 162019; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; agarose-fp
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                         Sequencing vector: M13; M77815; 100% of reads
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42802: contig of 10719 bp in length
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contig of 12693 bp in length
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80005: contig of 12223 bp in length
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(06699: contig of 26594 bp in length
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Consensus quality: 150998 bases at least 1040
Consensus quality: 150219 bases at least 030
Consensus quality: 160955 bases at least 030
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contig of 1476 bp in length
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f 2257 bp in length
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31983: contig of 6178 bp in length
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                                                                                                                                                              Chemistry: Dye-terminator Big Dye;
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                                                                                         Center project name: L8749
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                                                                                                          Center clone name: 69_
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5541: ~
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Query Match
Best Local Similarity
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Baldwin, J. Barna, N., Beckerly, R., Baguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Cadlangelo, M., Collins, S., Collymore, A., Cooke, P., Castle, A., Collangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardr, G., Hagos, B., Headord, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGrus, R., Morcandid, P., Marquis, N., McKernan, K., McLaughlin, J., Melfin, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollarav, V., Rilagy, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramani, M., A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Meeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                             Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               consists of B contigs. The true order of the pleces the new and their order in this sequence record is arbitrary, gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                             Submitted (15-NOV-1999) Whitehead Institute/MIT Center fo
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 1, 2000 this sequence version replaced gi:6573887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 183000; agarose-fp
Insert size: 178810; sum-of-contigs
Quality coverage: 6.8 in Q20 bases; sum-of-contigs
Quality coverage: 7.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                         repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap; version 0.960731
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Web site: http://www-seq.wi.mit.edu
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Location/Qualifiers
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/db_xref="taxon:9606"
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88113: cont
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61037: cont
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y,J., Levine,R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Dodge, S., Domlno, M., Doyle, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 aaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattcatcatt 264
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Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACO23371 48532 bp DNA HTG 14-FEB-2
Homo sapiens clone RP11-21D18, LOW-PASS SEQUENCE SAMPLING.
ACO23371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lander, E., Abraham, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 69.2; DB 71;
Pred. No. 0.38;
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32374 c 31805 g 55501 t
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Landers,T.
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17461: 18326: 19191: 20081:	or o	2502. Control 949 of 24422. contig 949 of 25286. contig 949 of 26173. contig 949 of 27055. contig	28036: contig 9ap of 9ap of 9ap of 29800: contig 9ap of 30670: contig	* 300/1 31009; contig of 999 bp in length * 31670 32564; contig of 895 bp in length * 32565 33435; contig of 871 bp in length * 33436 34363; contig of 871 bp in length * 33436 34363; contig of 898 bp in length * 33436 34363; contig of 988 bp in length	itg of 901 b of unknown itg of 867 b of unknown itg of 893 b of unknown itg of 898 b of unknown itg of 898 b		45009: control 45009: control 45881: control 46757: control 47645: control 48532: control 68532: control
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eters, R., Meldrim, J., 1, V., Morrow, J., Naylor, J O'Neil, D., Olivar, T.M., 1ra, V., Raymond, C., Santos, R., Schauer, S., 5 Cojanovic, N., Theodore, J., Tirrell, A., Theodore, J., Tirrell, A., Theodore, J., Tirrell, A., Theodore, J., Tirrell, A., Thoun, J., 21mmer, A. and	Center for Genom 41, USA	Genome Research	bled into the reads pletely useful for and allows deduced.	tii			
MCKETNAN,K., MCPheeters,R., b Miranda,C., Mlenga,V., Worrov T., O'Donnell,P., O'Neil,D., Pisani,C., Pollara,V., Ray, Stange-Thomann,N., Stolgnov, Stange-Thomann,N., Stolgnov, S.J., Tesfaye,S., Theodore,J J., Vassiliev,H., Viel,R., Vo.	Zody,M. Direct Submission Submitted (Lie FEB-2000) Whitehead Institute/MIT Center Submitted, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.denome.washington.edu/RM/RepeatMasker.html	Center: Whitehead Institute/ MIT Center for Gen Center code: WIBR Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu 	assen assen rate t is con ng is -rich to be hat th	mpletion. In the event the accession number will the accession number will go 6 869 bp in length of unknown length of unknown length of 882 bp in length is of 882 bp in length	unknown length of 871 bp in length unknown length of 901 bp in length unknown length of 870 bp in length unknown length of 864 bp in length unknown length unknown length unknown length	unknown length of 896 bp in length unknown length of 868 bp in length unknown length of 874 bp in length unknown length of 859 bp in length unknown length of 856 bp in length of 856 bp in length	of 860' bp in length unknown length length of 881 bp in length of 883 bp in length of 883 bp in length unknown length of 872 bp in length of 872 bp in length of 872 bp in length unknown length of 872 bp in length unknown length of 886 bp in length
rk,A., McKern va,T., Mirand Connor,T., O' erre,N., Pisa erre,N., Rothang Cer,B., Stang Talamas,J., gillo,J., vas	on EB-2000) Whit harles Street e identified Green, P. (Green, P. Asshington	Genome Center tehead Instit: WIBR ttp://www-seq quence_submis Project Infor ect name: 139 e name: 21_D_	cord contains ads that have of N are used in which they wrpass sequent lones that man ionships among	updated, the updated, the 869: contig gap of 1715: contig gap of 2597: contig gap of 1705: contig gap of 1	3468: contig 949 of 4369: contig 949 of 949 of 949 of 940 of 940 of 940 of 940 of 940 of	gap of gap of gap of contig gap of gap of contig contig gap of	12188: contig gap of 13069: contig gap of 13952: contig gap of 14829: contig 15701: contig gap of 15701: contig
McEwan, P., McGurk, A., McKernan, K., McPhemers, L., Mihova, T., Miranda, C., Mienga, Norman, C.H., O'Connor, T., O'Donnell, P., Opeterson, K., Plearre, N., Plaan, C., Polla, Riley, R., Spencer, B., Stange-Thoman, N., Severy, P., Spencer, B., Stange-Thoman, N., Travers, M., Trigillo, J., Vassillev, F., Wu, X., Wyman, D., Ye, W.J., Young, G., Zain, Wu, X., Wyman, D., Ye, W.J., Young, G., Zain,	Zody,M. Direct Submission Submitted (14-FEB Research, 320 Chan All repeats were Smit, A.F.A. & Gre http://ftp.genome	Center: Whi Center code Web site: h Contact: se	* NOTE: This record contains 55 indiv- sequencing reads that have not been contigs. Runs of N are used to sepa- and the order in which they appear arbitrary. Low-pass sequence sampli- identifying clones that may be gene overlap relationships among clones in However, it should not be assumed the		2598 3469 4370 5240		11329 11 12189 1 13070 1 13953 1 14830 1 15702 1
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Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
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                                                                                                                                                                                                                                  69 taaatattaatcattatttttaagatattaattaagaaattaaagatttaaaagaaa 128
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a working draft's sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000 this sequence version replaced gi:6652499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 204951)
an, R.W., Oin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
                                                                                                                                                                                              ö
                                                                   /clone_lib="RPCI-11 Human Male BAC"
9672 c 9208 g 15109 t 332 others
                                                                                                                                                                                          0; Mismatches 113; Undels
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gap of unknown length
contig of 14207 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 57789 bp in length
gap of unknown length
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                                                                                                                                                           Score 69; DB 51;
Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   onway, A.B. and Davis, R.W.
Lasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROGRESS ***, 13 unordered pieces.
                /organism="Homo sapiens
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         malaria parasite P. falciparum.
                                                  /clone="RP11-21D18"
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                                                                                                                                                         Query Match 5.3%;
Best Local Similarity 54.4%;
Matches 135; Conservative
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AC005505/c
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944 aaaataaaccttgggccttgtgctgactgagatggggtttggtgattacagaattttagc 1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1244 ctcctgttgtaaatttactgtttaggtactaactctaggcttgttgtgcagtttttgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1124 gggaattaatcccttccttcaaatccagtttgtttgtatatatgtttaaaaaatgaaact
                                                                                                                                                                                                                                                                                                                                 Score 69; DB 60; Length 204951;
Pred. No. 0.39;
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                                                                                                                                                                                                                                                                            2405 others
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 215; Indels
            bp in length
                                        bp in length
                                                                   length
                                                                                              bp in length
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length
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contig of 2442 b
gap of unknown l
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83609 a 19825 c 24530 g 74582 t
  unknown
                                                                    of 4058
                                         of 1611
                                                                                                                                                                                                                       /organism="Plasmodium/db_xref="taxon:5833"
                                                                                                                                                                                             Location/Qualifiers
           contig
gap of
contig
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                                                                                                                                    gap of
gap of
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Dictyostelium discoideum
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                                                                       2 (bases 1 to 975)
Kinmel,A.R. and Gollop,R.
Direct Submission
Submitted (28-JaN-1997) LCDB, NIH, 6/Bl-22, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 969 TITITITITATITICAAAAAAAAAAATIGATCTTITITATITATITATITATITATI 910
                                                                                                                                                                                                                                                                                                                                                                                                                          118 ttttaaaaaaatgtataaaattatattcatgatttttcatacatttgattttgataa 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Plasmodium falciparum
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 taaatatattittitttaatticitaaaaaatgitgoaagacacttattagacatagicit
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                                                                                                                                                                                                                                                                                                               Length 975;
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                                                                                                                                                      /organism="Dictyostelium discoldeum#
                                                                                                                                                                                                                                                                                                                                         0; Mismatches 181;
                                                                                                                                                                                                                                                                                                               DB 33;
Eukaryota; Dictyostellida; Dictyostellum.

1 (bases 1 to 975)

Kimmel, A.R. and Gollop, R.

CAR3 promoter of Dictyostellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                             Score 68.4; D
Pred. No. 2.2;
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                                                                                                                                                                                  /db_xref="taxon:44689"
                                                                                                                                 Location/Qualiflers
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                                                                                                                                                                        /strain="Ax-3"
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Best Local Similarity 49.4%;
Matches 177; Conservative
                                                                                                                                                                                                             /gene="CAR3"
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AC006278/c
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ORIGIN
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ribosomal RNA, Arpase, chlorophyll a aportotein; cytochrome; cytochrome b559; cytochrome b6; cytochrome f; cytochrome subunit IV; F-0-Arpase; Fl-Arpase; initiation factor; photosynthesis; photosystem II; ribosomal protein; ribosomal protein L16; ribosomal protein L20; ribosomal protein L21; ribosomal protein L21; ribosomal protein L21; ribosomal protein L23; ribosomal protein L21; ribosomal protein L23; ribosomal protein S12; ribosomal protein S13; ribosomal protein S14; ribosomal protein S15; ribosomal protein S19; riboso
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-Phe; transfer RNA-Pro; transfer RNA-Ser;
transfer RNA-Trp; transfer RNA-Tyr; transfer
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X04465.1 GI:11640
16S ribosomal RNA; 23S ribosomal RNA; 4.5S ribosomal RNA; 5S
                                                                                                                                                                                                                     is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
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Marchantiophyta, Marchantiales, Marchantiaceae, Marchantia
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2000 this sequence version replaced g1:6652497
                                         NOTE: This is a working draft's sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes
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Marchantia polymorpha chloroplast genome DNA.
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Pred. No. 0.65;
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Best Local Similarity
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of

238 rRNA 168

us-09-464-528-6.rge

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rpoA: homologous to E.coli beta
rpoB: homologous to E.coli beta'
rpoCl: homologous to E.coli beta'
rpoCl: homologous to E.coli beta'
50S subunit
rpl2: homologous to E. coli L2
                                                                                          12 (bases I to 121024)
Fukuzawa, H., Kohchi, T., Sano, T., Shiral, H., Umesono, K.,
Inokuchi, H., Ozeki, H. and Ohyama, K.
Structure and organization of Marchantia polymorpha chloroplast
genome. III. Gene organization of the large single copy region from
rbct to trnI(CAU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-OCT-1986) K. Ohyama, Research Centre for Cell and
Tissue culture, Faculty of Agriculture, Kyoto University, Kyoto
Structure and organization of Marchantia polymorpha chloroplast genome. I. Cloning and gene identification J. Mol. Biol. 203 (2), 281-298 (1988) 89068685
                                                                                                                                                                                                                                                                                                               Fine structural features of the chloroplast genome: comparison
the sequenced chloroplast genomes
Nucleic Acids Res. 19 (5), 983-995 (1991)
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rpl16: homologous to E. coli L20
rpl20: homologous to E. coli L21
rpl22: homologous to E. coli L22
rpl23: homologous to E. coli L23
i: homologous to E. coli L33
i: homologous to E. coli L33
i: homologous to E. coli L33
iii)
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photosystem II 32kd
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rbcL: large subunit of Ru
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Shimada, H. and Sugiura, M.
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Nucleotide sequence of Marchantia polymorpha chloroplast DNA: a region possibly encoding three FNNAs and three proteins including a homologue of E. coli ribosomal protein 14 M.
Nucleic Acids Res. 12 (24), 9551-9565 (1984)
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Agric. Biol. Chem. 49, 2725-2731 (1985)

Yamano, Y., Kohchi, T., Fukuzawa, H., Ohyama, K. and Komano, T. Nucleotide sequences of chloroplast 4.5 S ribosomal RNA from a leafy liverwort, Jungermannia subulata, and a thalloid liverwort,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kohchi, T., Shirai, H., Fukuzawa, H., Sano, T., Komano, T., Umesono, K., Inokuchi, H., Ozeki, H. and Ohyama, K. Irokuchi, H., Ozeki, H. and Ohyama, K. Structure and organization of Marchantia polymorpha chloroplast genome. IV. Inverted repeat and small single copy regions J. Mol. Biol. 203 (2), 353-372 (1988)
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Umesono,K., Shiki,Y., Takeuchi,M., Chang,Z., Aota,S., Inokuchi,H.
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Nature 322, 572-574 (1986)
(6 (base) 1 to 121024)
Fukuzawa, H., Kohchi, T., Shirai, H., Ohyama, K., Umesono, K.,
Coding sequences for chloroplast ribosomal protein S12 from the liverwort, Marchantia polymorpha, are separated far apart on the different DNA strands
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                                Yamano,Y., Ohyama,K. and Komano,T.
Nucleotide sequences of chloroplast 5S ribosomal RNA from cell
suspension cultures of the liverworts Marchantia polymorpha and
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irr. Genet. 14 (2), 147-154 (1988)
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FEBS Lett. 185, 203-207 (1985)
5 (bases 1 to 121024)
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Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 256172)
Hyman, R.W., Fung, E.L., Oin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
: segref@genoscope.cns.fr
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Hyman, R.W., Oln, E., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
Submitted (18-JUN-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
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                                                                                               Submitted (16-FBB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                           Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
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* NOTE: This is a "working draft' sequence. It currently

* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Conservative 15; Mismatches 117;
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Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
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Anopheles gambiae STS SP6 end of clone 06E14 of NotreDamel library
from strain PEST of Anopheles gambiae (African malaria mosquito),
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Culicoidea; Culicidae; Anopheles.
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                                                           ATPase F1 subunit epsilon
ATPase F0 subunit I
ATPase F0 subunit III
ATPase F0 subunit IV
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subunit of inner membrane
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  sm II G protein
subunit alpha
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ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, WY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's

Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

/organism="Drosophila melanogaster" /db_xref="taxon:7227"

source

FEATURES

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqréf@genoscope.cns.fr

Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilldae, Drosophila.

Drosophila melanogaster

ACCESSION VERSION KEYWORDS SOURCE ORGANISM 1 (bases 1 to 1101) Genoscope.

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Direct Submission

genomic survey sequence.

GI:4949849

AL069706.1 GSS. fruit fly. BP 191 91000 DATE CONTROLL WAS CARTIED OUT AS PART OF DETERMINATION OF THIS BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila The BDGP is constructing a physical map of the Drosophila construction construction

573 taatoggtaacattagactttcaaaatcatttttaacccctaaacagtaaatttgaagga 632 939 AWWWTWTTATTTTTTTTTTTTWTATWTWTTTATATWWWAAAAWAWWAAWWAA 880 879 ТТТТТИТТАТИАТТИАТТАТТАНАТТТТТТИТИТАТТИМТАТАТИМТИМТАТИТТТ 820 ctacacattgaccattgaaaagttcgttctcccatgggtaaccagatcaaactcacatcc 872 819 WAIWTATWTATTTATWTWTWTTWTATWTATAWWWTWWATWWWTAWAAWTATATAT 7.60 873 aaacataacatggatatctccttaccaatcatactaattattttgggttaaatattaatc 932 699 ITITITITITIMIAITIWAAATIATITAATIAWWAATWAWITATITIAATAAWIAATIAAAT 640 Gaps tctaaaaacaaaatttcatggcagcatgcctcagcccatgaaaaaaaccttataaaaatat Length 1101; Indels Query Match
4.4%; Score 95; DB 122;
Best Local Similarity 34.7%; Pred. No. 6.6e-07;
Matches 197; 'Conservative 100; Mismatches 270; 813 753 g qa. ô q a ö g õ g ö ò ç

1101 bp DNA GSS 04-JUN-1999 melanogaster genome survey sequence T7 end of BAC: of RPCI-98 library from Drosophila melanogaster (fruit

CNSODEVL Drosophila me) BACR29B23 of F

RESULT 1 CNSOOEVL/C LOCUS DEFINITION

ALIGNMENTS

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/clone="BACR29B23"

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BASE COUNT ORIGIN

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"Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
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- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila genome Project (BDCP).

The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osocgawa and Aaron Wammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Bufffalo, NY. The ilbrary is named RPCI-98 and was constructed by partial Ecold digestion of Drosophila DNA provided by the BDCP from the isogenic strain y2: cn bw sp, the same strain used for the BDCP's Pl and EST ilbraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope.- Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequence T7 end of BAC:
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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Determination of this BBC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, WY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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please see http://www.fruitfly.org The BDGP.Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order.individual BAC clones; the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)
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Submitted (02-JUN-1999) Genoscope - Centre National de
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Best Local Similarity 34.0%; Pred. No. 7.8e-06;
Matches 127; Conservative 92; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 928
/organism-"Drosophila melanogaster"
/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone="BACR27A24"
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                                                                                                                                  melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial NY. The library is named RPCI-98 and was constructed by partial EOSI Idigestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's Planary and EST libraries. A more detailed description of the library
- FRANCE (E-mail : segref@genoscope.cns.fr
                                   carried out as part of
Genome Project (BDGP).
                                                                                                                                                                                                                                                                     and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Determination of this BAC-end sequence was carried out as part
collaboration with the Berkeley Drosophila Genome Project (BDGI
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
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/db_xref-"taxon:7227"
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20.6%; Pred. No. 9.1e-06;
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN12P22 of DrosBAC library from Drosophila melanogaster (fruit
                                                     1545 tacctctcaaggtacttttcttctccctctaccaaatcctagattccgtggttcaatttc 1604
                                                                                                                                                                                                                                                                                     963 АААААААНЖИМИМИМИМИТТТТТТТТТТТТТТТТТААМИТТТАИТИМИНИТТТ 904
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Pred. No. 1.4e-05;
); Mismatches 159;
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/plasmid="pBeloBAC11"
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Web: www.genoscope.cns.fr.
Web: www.genoscope.cns.fr.
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfiy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Cantitute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. Or filters for hybridization from the BACPC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K08 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
attataattaaactgaaaacaatttggtatcaattcatatacatgcttagtaataaaatg 347
                                                                                                                                                        408 acaaattttgtcgttttcatggtgttggtctgaggaggatttggcactatagaactctcc 467
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila,
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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Drosophila melanogaster
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fly), genomic survey sequence.
AL059666
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Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                          Length 1101;
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                                                                                                             /organism-"Drosophila melanogaster"
/db.xref-"etaxon:7227"
/clone_lib-"RPCI-98"
/clone="BACR08f10"
                                                                                                                                                                                                                                                                                      3.9%; Score 84; DB 122;
llarity 18.5%; Pred. No. 4.6e-05;
Conservative 292; Mismatches 272;
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CNSODCS1 843 bp DNA GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR26H19 of RPCI-98 library from Drosophila melanogaster (fruit

CNS00CS1/c LOCUS DEFINITION

RESULT

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- Web: www.genoscope.cns.fr;
- Web: www.genoscope.cns.fr;
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library, and how to order individual BAC clones, the entire library, or
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       filters for hybridization from the BACPAC Resource Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inše
Pterygota; Neoptera; Endopterýgota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 843)
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/clone_lib="RPCI-98"
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Drosophila melanogaster genome survey sequence TET3 end of BAC # BAR058hll of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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/db_xref="taxon:7227"
/clone_lib="RPCI.98"
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Web: www.genoscope..cns.fr)

Letermination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) thtp://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC hibrary (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humanin) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence T7 end of BAC
BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
                                                   1154 cttcttgtgagtggtgtgggagtaggcaacctggcattgaaacgagagaaagagagtcag 1213
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                                                                                                    623 TITITITITIMWITAWATIAAAAWIAAAWAWIWITITATIAAAATITWIWITAAAAATIAAAA 564
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Pterzyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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llarity 33.6%; Pred. No. 7.2e-05;
Conservative 90; Mismatches 133;
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                                                                                                                         1214 TATWATWAAWW 1224
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk · This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                  Drosophila melanogaster genome survey sequepce SP6 end of BAC
BACNISC18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106171
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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35.3%; Pred. No. 0.00011;
1ve 93; Mismatches 180; Indels
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/plasmid="pBeloBAC11"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 928)
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L; Mismatches 154;
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/clone_lib="DrosBAC"
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Drosophila melanogaster
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -http://www.edgp.ebl.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-JUL-1999) Genoscope · Centre National de Sequencage ·
BP 191 91006 EVRY cedex · FRANCE (E-mail · segrefégenoscope.cns.fr
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                677 TATTWITTTTTTWITTWITTWIATATAAWAWTAWAAWAWAWAIATIAIATWAWAIAITTW
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Pred. No. 0.00013;
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="brosBAC"
/clone="BACN15C13"
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CNS016E1/c
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                                                                                                                                                                                                                                                                                                                                    ACCESSION
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JOURNAL
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KEYWORDS
SOURCE
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Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Pictude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence T7 end of BAC abchild: of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ALI03735
                                                                 1098 tacaaaagcattcatcatttaatacattaaaaaaatatttaatactaacagtagaatcttc 1157
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                                                                                                      1010 ITTTTTTTTAWTTTTATTAWTWATAAAAAATWTTAMCTATATWMAATAAAATATTT
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1043)
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41.2%; Pred. No. 0.00015;
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Search completed: September 2, 2000, 00:25:01 Job time: 4325 sec

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Sequence Sequence Sequence.

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ALIGNMENTS

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COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE ADDRESS:
                                                                      US-08-181-271A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
AFTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)836-9300
TELEFAX: (703)835-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                         US-08-449-31
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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INFORMATION FOR SEQ ID NO: 14'
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                                                                                                      September 2, 2000, 01:57:31 ; Search time 111.97 Seconds
(without alignments)
2659.716 Million cell updates/sec
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Patent No.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                   Compugen Ltd
                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -487-826B-13
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-08-446-855A-1
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapëxt 1.0
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Maximum DB seq length: 1000000
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Perfect score:
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No.
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Pred. No.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
                                                                                                                         Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                   Peterson, David S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.68;
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NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.6'
Best Local Similarity 47.7'
Matches 164; Conservative
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                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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JS-08-487-826B-13
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US-08-487-826B-13
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APPLICANT:
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                  Length 7218;
                Ouery Match 3.6%; Score 78; DB 1; Length 721
Best Local Similarity 3.8%; Pred. No. 1.2e-06;
Matches 15; Conservative 241; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATENT NO. 5231168
APPLICANT: DZIEGIEL, MORTEN:BORRE, MARTIN:JEPSEN, SOREN:VUUST, JENS:RIENECK, KLAUS:WIND, ANNETTE:JAKOBSEN, PALLE H. TITLE OF INVENTION: MALARIA ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57.2; DB
Pred. No. 0.008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1766 atgagaaataaaatcattttttttttatttcaa 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1431 YYYYGTACCAATTCTTCTATCTCTTTAACTA 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
FILING DATE: 18-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.6%;
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5231168-1
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APPLICANT: Wellems, Thomas E. APPLICANT: Wellems, Thomas E. TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                            ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
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1149 agaatettettgtgagtggtgtgggagtaggcaacetggeattgaaacgagaaagaga 1208
                                         1504 ATATTAATATTAGTAACCACCTAGATAAATTAGAGAGAAACGTAGAACATACCAAAAAA 1563
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                                                                                                                                                                                                                                                                                                                         Biocontrol of Fungal Soilborne Pathogens
by Pythium oligandrum
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                                                                                   1564 ATTAGAACAAAAGAATATTACAAAAATAATAAAATTAAATTA 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,722
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                 Sequence 5, Application US/08731722
Patent No. 5961971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
RESTSTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELECOMMUNICATION INFORMATION
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: DNA (genomic)
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                                                                                                                                                                                                                                                                                                       APPLICANT: Martin, Frank N. TITLE OF INVENTION: Biocont TITLE OF INVENTION: by Pyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; INDIVIDUAL ISOLATE: 23-5
US-08-731-722-5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1186 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 2.5
Best Local Similarity 59.3
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1084 agtettgtt 1092
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|AAATTAATT 411
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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                                                                                                                                                                                                                   JS-08-731-722-5/c
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2802 AATIGAAACITAAICIAITITITAIGIITITAAITITAITAITITITAAAATAITITAAA 2861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2982 atatattaaataattaatgtataatttatataaaaaatcaaaggagcttataaattatga 3041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; LOCATION: 3770.4013

OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from OTHER INFORMATION: plasmid RP4"
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                                                                                                                                   Expression System for Clostridium Species
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/056,075
                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          Quarles & Brady
South Pinckney Street
Sequence 1, Application US/09056075 Patent No. 5955368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELECOMMUNICATION INFORMATION TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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50.8%;
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Best Local Similarity 50.8'
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                            OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                       53701-2113
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                                                                                                                                                                                                                                                                       Madison
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                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                APPLICANT
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15642 TITTATAATCATITITITITATATAAATITITITITAATITITITATATATTITITITAAAT
                                                                                                                                                                                                                                            1910 catacattccttaggcttcaattttattcgagtataggtcacaataggaattcaaacttt 1969
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                                                                                                                                                                                                                                                                               2090 tttgctctcctgttgtaaatttactgtttaggtactaactctaggcttgttgtgcagttt 2149
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F: One Liberty Place 46th Floor
Philadelphia
                                                                                                                                  : Improved Plasmid Vectors for Cellular : Slime Moulds of the Genus Dictyostellum
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19920625
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Patent No. 5389526
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                  Weilems, Thomas E.
ZENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
ZENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1790 tatticaaaataaacctigggcctigtgctgactgagatggggttiggtgattacagaat 1849
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 3042 TTATTTCCAAAGATACTAAAGATTTAATTTTTCAATTTTAACAATACTTTTGTAATAT 3101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
                                                                                                                                                                                                                                                                                                                                                                                                                                   620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53.6; DB
Pred. No: 0.049
0; Mismatches
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10-SEP-1993
                                                                                                                                                                        lication US/08487826B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newport Beach
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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Best Local Simi
Matches 221;
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US-08-487-826B-13
                                                                         3102 T 3102
                                        424 t 424
                                                                                                                                                                        Sequence 13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22201-4714
ORGANISM: HOMC
: IMMEDIATE SOURCE:
: CLONE: Rh 32
US-08-883-795A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .446-855A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                    Query Match
                                                                                                                                                                                                                                              963 aaagattttttaaaaaaaatgtataaaattatattattcatgattttcatacatttgatt 1022
                                                                                                                                                                                                                                                                                                                                                                                                          1023 ttgataataaatatattttttttaatttcttaaaaaaatgttgcaagacacttattagaca 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2893 GGGACGATGTAATATCATATGATTCAAAATTAAAAGTTATTAACAAATATGTAAAAAT 2952
                                                                                               783 cagocoatgaaaaaaacottataaaaatatotacacattgacoattgaaaagttogttot 842
                                                                                                                                                                                                                                                                                                      723 agatgtaactaaaccaatatttattttattttctaaaacaaaatttcatggcagcatgcct 782
                      Gaps
                                                                                                                                                                              2653 GAATIGAAAAAAACAGAAAGITATATATTTACCCCCTTTAATTTTTTAAAACTTTTGA
                                                                                                                                                                                                                                                                                                                                              2773 AAATTGATTAAGATAAAGTTATATGTTTGTATTTAATAAAATAGTTTAGTTTAAAAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Recombinant DNA Molecules and Expression TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSOR
  46.7%; Pred. No. 0.045;
tive 0; Mismatches 193; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/883,795P
FILING DATE: 27-JUN-1997
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REFERENCE/DOCKET NUMBER: 7841-062
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YSTEM: PC-DOS/MS-DOS
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  Best Local Similarity 46.79
Matches 169; Conservative
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LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ORIGINAL SOURCE:
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1045 taatttettaaaaaatgttgeaagaeacttattagaeatagtettgttetgtttaeaaaa 1104
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APPLICANT: Flores, Maria V
APPLICANT: Flores, Maria V
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
CORRESPONDENCE: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                              1105 gcattcatcatttaatacattaaaaaatatttaatactaacagta 1149
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 3;
Pred. No. 0.088;
                                       0; Mismatches
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TORNEY/AGENT .... 435
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REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
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                  55.1%;
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                  Best Local Similarity 55.1
Matches 124; Conservative
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INFORMATION FOR SEQ ID NO:
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FILING DATE:
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                                                                                                  1023 ttgataataaatatatttttttaatttcttaaaaaatgttgcaagacacttattagaca 1082
                                                                                                                                                                                                                                     1083 tagtottgttotgtttacaaaagcattcatcatttaatacattaaaaaatatttaatact 1142
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FITLE OF INVENTION: Recombinant DNA Molecules and Expression
FITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
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 Indels
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 Mismatches 135;
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Pred. No. 0.084;
); Mismatches 243;
                                                                                                                                                                                                                                                                                                      1143 aacagtagaatcttcttgtgagtggtgt 1170
                                                                                                                                                                                                                                                                                                                                      537 AATTATAGGAACCACAATATTGGGGAGT 510
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27-JUN-1997
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NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,2
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OPERATING SYSTEM: PC-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 361-1398 (NFORMATION FOR SEQ ID NO:
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 Conservative
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Best Local Similarity 46.0
Matches 200; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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CLONE: Rh 32
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ORIGINAL SOURCE:
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Matches 133;
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APPLICANT:
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942 aagatattaattaagaaattaaaagattttttaaaaaatgtataaaaattatatttca 1001
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                                                                                                                                                                                                                                                                                                                                               378 GTAATTATAAACATTTTAAATTATAAATATGTAATTATAAACATTTTAATTATAAAATAT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                318 GTAATTATAAACATTTTAAATTATAAATATTTAAATTATAAACATTTTAAT-TATAAAATA 260
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                                                                                                                                                                                                                                                 882 atggatatctccttaccaatcatactaattattttgggttaaatattaatcattatttt 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 ATATTGAATTATAAAATATGTAATTATAAATACTTTAATTATAAAATATGTAATTATAAA 499
                                                                                                                                                                                                 822 gaccattgaaaagttcgttctcccatgggtaaccagatcaaactcacatccaaacataac 881
762 aaatttcatggcagcatgcctcagcccatgaaaaaaaccttataaaaatatctacacatt
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by Pythium oligandrum
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2421 N.W. 41st Street, Suite
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3933 base pairs
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SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                            965
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                                                                                                                                                                                                                                                        965 agattititaaaaaaatgiataaaattatattootgattiticatacattigatti 1024
                                                                                                                                                                                                                                                                                                                                        1025 gataataaatatatttttttaatttcttaaaaaaatgttgcaagacacttattagacata 1084
                                                                                                                                                                           505 ATTATTTATTTCTTATTAAAATATTATGATTATTATTAAAGTAGÄÄTÄAGG--ATTACA 562
                                                                                                                                                                                                                                                                                    APPLICANT: Martin, Frank N.
TITLE OF INVENTION: Biocontrol of Fungal Soilborne Pathogens:
TITLE OF INVENTION: by Pythium oligandrum
UNUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                Length 3933;
                                                                                                                                                                                                                                                                                                                                                                                                                   1085 gtcttgttctgtttacaaaagcattcatcattaatacattaaaaaatat 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                       683 GTAGAATIGAGAGAAATAATAGTICTAATITACTITATATAATAT 732
                                                                                            Ouery Match 2.4%; Score 51.2; DB 4; Length 3 Best Local Similarity 54.3%; Pred. No. 0.11; Matches 125; Conservative 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-731-722-3/c; Sequence 3, Application US/08731722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WhitLock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; INDIVIDUAL ISOLATE: 1986-41 US-08-731-722-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,965
                  1986-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Tinear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3933 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352-375-81
352-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
US-08-731-722-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 32606-6669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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Length 3933;

Score 51.2; DB 4; Pred. No. 0.11; 0; Mismatches 103;

Query Match 2.4%; Best Local Similarity 54.3%; Matches 125; Conservative (

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3429 ATTATTTATTTATTAAAATATTATGATTATTTATTAAAGTAGAATAAGG - ATTACA 3372
                                                                                                                          3371 ATTICIGITAAAAAAAAAAACCITICICIATIGAAGAAITITITATAGCIACIGITTA 3312
                                                                                                                                                                                                                   agattttttaaaaaaatgtataaaattattattcatgattttcatacattgatttt 1024
                                                                                                                                                                             1025 gataataaatatattttttttaatttcttaaaaaaatgttgcaagacacttattagacata 1084
DNA Sequence Encoding Surface Protein of
                                                                                                                                                                                                                                                                 1085 gtcttgttctgtttacaaaagcattcatcatttaatacattaaaaaatat 1134
                                                                                                                                                                                                                                                                                                            3251 GTAGAATTGAGAAATAAATACTTCTAATTTACTTTATATTAATAT 3202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cryptosporidium Parvum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: USDA-ARS-OTT-NCAUR
: 1815 N. University Street
Peoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/229,393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08229393
Patent No. 5591434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309)-681-6515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jenkins, Mark C
APPLICANT: Fayer, Ronald
APPLICANT: Tilley, Michael
APPLICANT: Upton, Steven J
TITLE OF INVENTION: DNA Sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 602 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
5-08-229-393-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61604
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1869 gtacttgtttgtctgtagttttgttttgtttcttgtttctcatacattccttaggcttc 1928
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                                                                                                    1809 ggccttgtgctgactgagatggggtttggtgattacagaattttagcgaattttgtaatt 1868
                                                                                                                                                                                                                                                                                                                                                                                                           1929 aattttattogagtataggtoacaataggaattoaaactttgagoaggggaattaatoo 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 CGAATTATTAAAGAAAAGGGGAATACAGTTTCCTGATTCTTTGAGATGAATTGCAACACA 361
                                                                                                                                                                                                                                                 540 GCTATTTGGATTTTATTTATGGGTTTGGAAAAACAAATCCAGAATAAATGAAATTCCT 481
                                                                                                                                                                                                                                                                                                                                                        360 ATTGTCGGAATCGCTGATTCCAGCACTACTTTCAACTCTAGAAAGCTCTTCCTTTGAATA 301
                                                                                                                                                 600 TITITITITITITITITAATCAAAATATTTTATTAATTCTCTCCCTGTGATTGAAGAAAA 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 TAATAATTGGTGGATTTCATCCAAAGCAATATTTCTGCATTTTCCATCTCCAGAAAGCGA 241
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Length 602;
Score 50.8; DB 1; Length 602
Pred: No. 0.099;
0; Mismatches 197; Indels '
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STREET: 1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleotide sequence enc
TITLE OF INVENTION: phosphate synthetase II
UNUBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vanderhye PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart, Thomas S
Flores, Maria V
O'Sullivan, William J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08446855A Patent No. 5849573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
* REFERENCE/DOCKET NUMBER: 47
FELECOMMUNICATION INFORMATION:
  2.3%;
ilarity 46.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTORNEY/AGENT INFORMATION:
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                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                       Matches 169;
     Query Match
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8633 ATTITIGITATATACAAATTITATTTATTCACTCATATGTATAAACCAAAATGGTTTT 8692
                                                                                                                                                                                                                                                                                                                                                                                1032 aatatattttttttaatttcttaaaaaatgttgcaagacacttattagacatagtcttgt 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             852 aaccagatcaaactcacatccaaacataacatggatatctccttaccaatcatactaatt 911
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                            Length 8920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or Relating to Organic
                                                                                                                         0; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                     Score 50.6;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van Grinsven J., Martinus Q.
De Haan, Petrus T.
Gielen L., Johannes J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US 08/032,235
17-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/764,100 FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: GB 9206016.9 FILING DATE: 19-MAR-1992 TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FITLE OF INVENTION: Improvements FITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08764100 Patent No. 5773700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 5773700ris, Allen E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sandoz Agro, Inc
975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldbach, Robert W
                                                                                       Query Match 2.3%;
Best Local Similarity 47.6%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peters, Dirk
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
US-08-446-855A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8813 TTTTTTAAAAA 8825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94304
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REFERENCE/DOCKET NUMBER: 137-1061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
TELEPHONE: (415) 367-1125
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                TOPOLOGY:
US-08-764-100-16
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Gaps ó Length 473; Score 50.2; DB 2; Length 4 Pred. No. 0.12; 0; Mismatches 103; Indels Ouery Match 2.3%; Best Local Similarity 52.1%; Matches 112; Conservative

1042 ttttaatttettaaaaaatgttgcaagacacttattagacatagtettgttetgtttaca 1101

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Search completed: September 2, 2000, 01:59:26 Job time: 8330 sec

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Borrelia burgdorfe Continuation (4 of Orpinomyces cellul Orpinomyces cellul Carbamoyl-phosphat Malaria-specific 9 SERP gene. Recombi Borrelia burgdorfe Continuation (7 of Shuttle vector pMU CDNA encoding plas Borrelia burgdorfe Borrelia burgdorfe	<pre>apoptosis; resistance; tadenovirus; cancer; inflammation;</pre>	resistant virus-sensitive	we see the following ways and a populary of diseases for or where the he recombinant viruses e applied to cancer he treatment of and apoptosis induction eases. Prior arts have tor capable of ced into animal cells, cause the period of shorter than that thing in failure to poptosis associated cell line (having and and overcomes the sus of the rus shorter was gene, and	101
X20253 T58840_3 V37413 V29477 062924 N81157 062299 X20299 X20299 X21209_06 011712 T41852 X203361	rd; DNA; 6644 BP. (first entry) of the plasmid pRx-ires-bsr. bsr; viral vector; expression; apopt bc-x1; FLIP; survivin; IAP; ILP; adesease; graft rejection reaction; inflidease; ss.	ive cell	The recombinant viruses generated are capable of expressing apoptosis associated genes. These can then be used in a variety of diseases for which the induction of apoptosis, is therapted in a variety of diseases for inhibition of harmful apoptosis, is therapted. There there the recombinant viruses are useful as vectors for gene therapy which can be applied to cancer autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the plasmid pfar-ires-bsr, which contains the base sequence of the plasmid pfar-ires-bsr, which contains the cowpox virus bsr gene, and is used in an example from the present invention.	5 A; 15/5 C; 1424
52.4 2.4 100000 1 52.2 2.4 1826 1 52.2 2.4 1826 1 52.2 2.4 1826 1 51.8 2.4 3975 1 51.8 2.4 26811 51.8 2.4 26811 51.8 2.4 3138 1 51.2 2.4 3138 1 51.2 2.4 3789 1 51.2 2.4 3789 1	1 181; standa 181; 181; 181; 180; 180; 180; 180; 180;	08-SEP-1998; J04010. 08-SEP-1997; JP-259235. (RPRG-) RPR GENCELL ASIA PACIFIC INC. HAMMADA H. WPI, 99-243728/20. New apoptosis-resistant virus-sensitive cell Example 1; Page 38-41; 51pp; English. The present invention describes an apoptosis-	The recombinant viruses ge associated genes. These can which the induction of apoginhibition of harmful apopiare useful as vectors for autoimmune diseases and grautoimmune diseases and grates arountered the problem whe expressing an apoptosis assisted to replicate and in the required to replicate and gottime required to replicate and gottime required to replicate and gottime a recombinant virus gene. In this invention an apoptosis resistant gene in plasmid parties and recombinant virus gene. In this invention an apoptosis resistant gene in plasmid parties and researched.	equence 6644 BF; ZIO
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. nucleic search, using sw model September 2, 2000, 01:56:29; Search time 161.21 Seconds (without alignments) 3360.002 Million cell updates, US-09-464-528-14 1 atcgatagagacatgttattgtttttgaagtataaagatg 2165	Gapop 10.0. Gapext 1.0 311585 seqs, 125096042 residues hits satisfying chosen parameters: tength: 0 length: 1000000 : Minimum Match 0% Maximum Match 100% Listing first 45 summaries N_Geneseq_36:*	o. is the number of results ceater than or equal to the derived by analysis of the tearly analysis of the tearly submy Query	3.0 6644 1 x33181 Base sequence of 7372 1 x33182 Cowpox virus 3.0 7372 1 x33184 Base sequence 3.0 7372 1 x33184 Base sequence 3.0 7397 1 x33184 Base sequence 3.0 7397 1 x33184 Base sequence 3.0 7395 1 41852 Base sequence 3.0 81864 1 N71405 Base sequence 3.1 16000 1 x20246_05 Base sequence 3.1 160000 1 x20246_05 Base sequence 3.1 160000 1 x20246_05 Base sequence 3.1 160000 1 x20246_05 Base sequence 3.1 1600000000000000000000000000000000000	6 2.6 16/1 1 024134 50 KD subun 4 2 5 4590 1 N60472 Seguence en
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Sequence encoding Pythium oligandrum Human 3' apolipopr Sequence encoding PNRX30 xylanase cD Staphylococcus aur

Plasmodium var-7 g Sequence of autono Borrelia burgdorfe Continuation (4 of Human 3' apolipopr MS-Le1610 Vector.

X20251 X20248_03 T31530 Q55185

sequence encoding

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cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction
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Example 2; Page 41-45; 51pp; English.
The present invention describes an apoptosis-resistant virus-sensitive
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                                      gaaactctactctttttaatatctgcggaatacgcgttggactttcagatctagtcga
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(RPRG-) RPR GENCELL ASIA PACIFIC INC.
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expressing an apoptosis-associated gene is introduced into animal cell the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having a apoptosis resistant gene introduced is established and overcomes problem. The present sequence represents the base sequence of the plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and is used in an example from the present invention. Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T;
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ID X33180/C
AC X33180;
DT 25-JUN-1999 (first entry)
DE Cowpox virus bsr full length gene sequence.
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The present invention describes an apoptosis resistant virus-sensitive cell into into which an apoptosis resistant egene has been introduced.

Cell line into which an apoptosis resistant egene has been introduced.

The recombinant viruses generated are capable of expressing apoptosis.

Ssociated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis by gene transfer, or where the cancer the are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the cowpox virus bsr gene which
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Cowpox virus; bsr; viral vector; expression; apoptosis; resistance crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
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Pred. No. 0.0084;
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(RPRG-) RPR GENCELL ASIA PACIFIC INC.
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The recombinant viruses generated are capable of expressing apoptosis-
associated genes. These can then be used in a variety of diseases for
which the induction of apoptosis by gene transfer, or where the
inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
are useful as vectors for gene therapy which can be applied to cancer
therapy for destroying cancer cells selectively, the treatment of
autoimmune diseases and graft rejection reaction, and apoptosis induction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of the required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3: Page 46-49; 51pp; English.
The present invention describes an apoptosis-resistant virus-sensitive
cell line into which an apoptosis resistance gene has been introduced.
                                                                                                                                                                                                            ttgctctcctgttgtaaatttactgtttaggtactaactctaggcttgttgtgcagtttt 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene. In this invention an apoptosis-resistant 293 cell line (having a apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid pRx-Bcl 2-1-hCD 25, which contains the human Bcl-2 gene, and is used in an example from the present invention.

Sequence 7996 BP: 2463 A; 2015 C; 1829 G; 1689 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Base sequence of the plasmid pRx-Bcl 2-i-hCD 25. Cowpox virus, bsr; viral vector; expression; apoptosis; resistance; cmmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
aaacttttgctttaaattctattataacttttttatggcaaaaatttttgcatgtgtct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New apoptosis-resistant virus-sensitive cell
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ID X33184 standard; DNA; 7996.BP.
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WO9913073-A2.
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The CS protein is produced during the merozoite stage of the malaria parasite. The CS-related protein can be used to produce vaccines. The Abs can be used for the purificn. of the polypeptides. The vector may be a recombninant virus, esp. baculovirus or the peptide
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                         ttagcgaattttgtaattgtacttgtttgtctgtagttttgttttgttttgttttcttcttgtttctc
                                                                                                                                                                                                                                                                                           1911 atacattccttäggcttcaattttattcgagtataggtcacaataggaattcaaactttg 1970
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                                                                                                                                                                                                    1791 atttcaaaataaaccttgggccttgtgctgactgagatggggtttggtgattacagaatt
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                                                           gaaactctactcttctttaatatctgcggaatacgcgttggactttcagatctagtcga
                                                                                                                                                                                                                                                                                                                      Fragments of the peptide preferably contain a conserved sequence
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Sequence encoding a circumsporozoite (CS)-related protein
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Plasmodium falciparum; malaria; vaccine;
Plasmodium falciparum T.9/96.
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Robson K, Hall J, Hallowes J, Sadler
WPI; 90-083478/11.
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312. .1988
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e.g.residues 244 to 291 and more particularly a polypeptide selected from the following group:
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Pred. No.
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                  the following group:
A) WDBWSPCSYTCGKGTRSRR
B) WDBWSPCSYTCGKGTR
C) EWSPCYTCGKG
D) PCSYTCGKG
E) WSPCSYTCG
See also Q0204
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les 427; Conser
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A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte
membrane protein 1 (PfEmpH) or active fragments or analogues of that
protein can be used in the treatment or prevention of symptoms of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                   20-FEB-1997 (first entry)
CDNA encoding Plasmodium falciparum erythrocyte membrane protein.
Plasmodium falciparum; erythrocyte membrane protein; malaria;
detection; identification; treatment; prevention; parasite; ss.
Plasmodium falciparum MC type.
                       New Plasmodium falciparum erythrocyte membrane proteins - used develop products for the diagnosis, treatment or prevention of malaria parasite infections
                                                                                                                                                                                                                                                                                                              /transl_except= AAC encodes Aspartic acid 3461. .3463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_mxcept= GGA encodes Tryptophan
7754. .8478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encodes Asparagine
                                                                                                                                                                                                            'product - Erythrocyte membrane protein
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                                                                                                                                                                                                                                                                                                                                               except GAA encodes Glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_except* ATA encodes Histidine
                                                                                                                                                                                                                                             transl_except= GTA encodes Tyrosine.
56. .658
                                                                                                                                                                                                                                                                                                                                                                                /transl_except= CCT encodes Arginine 6254. .6256
                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_except- ATA encodes Tyrosine
                                                                                                                                                                                                                                                        /transl_except= ATT encodes Leucine
2909. .2911
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P-PSDB; W00384.
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                                                                                                                                                                          Location/Qualifiers 326. .9497
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                                                                                                  T41852 standard; DNA; 9789 BP
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6257. .6259
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26-APR-1996; U05798.
27-APR-1995; US-430908.
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11D 74
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CD DE CD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMPI gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different P. falciparum strains. Antibodies specifically immunoreactive with the PfEMPI polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the PfEMPI protein of the MC type of Plasmodium falciparum. An.
                                                                                                                                                                                                                                                                         alternative, truncated version of the coding sequence (a cDNA clone) is given in T41853.
Sequence 9789 BP; 4061 A; 1393 C: 1817 C: 2000 m.
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include secretory signal sequences that are native or foreign to
heterologous polypeptide(s), such as chymosin or glucoamylase.
Disclosure: Fig 13A-13B, 50pp; English.
The sequence represents the A. nidulans ANS-1 sequence which is
fincluded in the construction of transformation vectors for
recombinant protein expression and secretion from a filamentous
fungus host. The sequence increases the transformation efficiency
of the vector. This illustrates the main claims of the patent,
which provide a vector containing (i) DNA encoding a heterologous
polypeptide (chymosin, prochymosin, prochymosin, prochymosin, prochymosin, prochymosin, prochymosin, prochymosin, prochymosin, niger glucoamylase, Humicola grisea glucoamylase or M. miehei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ttttttaaaaaaatgtataaaattatattattcatgattttcatacatttgattttgat
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filamentous fungus (Aspergillus, Trichoderma, Neurospora,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%; Score 60.2; DB 1;
ilarity 48.2%; Pred. No. 0.064;
Conservative '0; Mismatches 183;
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Aspergillus nidulans ANS-1 partial sequence.
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Berka RM, Cullen D, Gr
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29-AUG-1985; US-771374.
07-JUL-1986; US-882224.
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Best Local Similarity
Matches 170; Conserv
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                                                                                                                                                                                                                                                       ttcatcattttctaaccaaacca-----atcttatatgttcttcaaattagaact 276
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example: Fig 13: 45pp; English.

A DNA sequence coding for a heterologous polypeptide which can be expressed in and secreted from filamentous fungl is claimed. Pref. the DNA sequence codes for bovine preprochymosin, M. meihei preprocarboxyl protease or A. niger preprocampulase. Also new are vectors consisting of the DNA sequence plus an operably-linked signal sequence. The vectors may also include a sequence which
Podospora, Endothia, Mucor, Cochiobolus or Pyriclaria, especially and indilans. A. awamori or T. reesei) transformed with the vector for recombinant protein (enzyme) production.

Sequence 1864 BP, 819 A, 193 C, 120 G, 732 T,
                                                                                                                                                                                                                                                                                                               tgaaattattaattaattaaactgaaaacaatttggtatcaattcatatacatgctta
                                                                                                                                                                                                                                                                                                                                                                     gtaataaaatgcgataattaattgataaatctgcaaaagattttacaaatatctttcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENENCOR INC.
Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
WPI: 87-095049/14.
New DNA sequences for expressing polypeptide in filamentous fungi
New DNA sequences for expressing molypeptide in filamentous fungi
New DNA sequences for expressing polypeptide in filamentous fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transformation efficiency. Aspergillus expression vector;
                                                                                                                 10;
                                                                                     Length 1864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          732 T;
                                                                                 2.8%; Score 59.6; DB 1; Length 1 51.9%; Pred. No. 0.078; vative 0; Mismatches 144; Indels
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Sequence of ANS-1 which increases
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                                                                                                                                                                                                                                                                                                                                                                                                                          397 aaaaattaataacaaatttt 416
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                                                                                                              Conservative
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29-AUG-1985; US-771374.
07-JUL-1986; US-882224.
                                                                                                   Similarity
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Matches 166;
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1016 tttgattttgataataaatatatttttttaatttcttaaaaaatgttgcaagacactta 1075
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                                                      1494 GAGNITIAITATIATINNNNIAGAGIAITITITAIAGITITCTIAAGIAATITATINITAGNIT
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                                                                                                                               364 aatctgcaaaagattttacaaatatctttcagaaaaaattaataacaaattttgtcgttt
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X20251 ID X20251 standard; DNA; 53585

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126 aattagaattttttttatcaataaatattaatttattagttttattagaaatattaatta 185

2.7%; Score 59; DB 1; Length 1864; 42.8%; Pred. No. 0.097;

0; Mismatches 583; Indels

Best Local Similarity 42.8 Matches 452; Conservative

Query Match

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Gaps . Score 58.8; DB 1; Length 53585; Pred. No. 0.11; 0; Mismatches 242; Indels 1; 2.7%; llarity 46.9%; Conservative

19266

7001 G;

8081 C;

19235 A;

taacccctaaacagtaaatttgaaggacaaaaataatatttttcaaatttgatagactat 665

tttttttttgtaatttgacgaaccaaaaccagatttatcctgaatttaggaaccacaga 725

33069 CTTAAATATTTCAAACTGAGCTTTTTTTCAAAGTCAAAATTATGCTTCCAAAAGCATTA- 33127 tgtaactaaaccaatatttattttattttctaaaacaaaatttcatggcagcatgcctcag 785

CAATTAAAAAAATCAAAGTTTGAGAACAAAAATATAGAAAAAATCTGTTTTTCATAATAG 33187 33128

33188 ACTCCTTAGTGGTAAAATAATAAATTAAATTATAAATCATATCAATAATATTTTCCAA 33247 atgggtaaccagatcaaactcacatccaaacataacatggatatctccttaccaatcata g

33248 AAAAATAAACTTTAAAAAAATTTTTCAAAATCTTTAAAAGATTGAATATTAATTTATA 33307 g ò

33308 TTTTTTACAAAATTTGCATTTTTAATATAAAAATTTAATTGTTTTAAATATTTTAATTTTA 33367 gattttttaaaaaaatgtataaaaattatattattcatgatttttcatacatttgattttg 1025 g

1026 ataataaatatttttttttaatttcttaaaaaatgtt 1063

33368 ATATTTATTTATTTTATTTTAATATTTAATATT 33405 a

X20248 to X20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for

burgdorferi polynucleotid X20248 36325 TCTCTTTCTGTTTTGAATTTGCTTATAAATTTTTTGTAACTTTCAGAAAAATTTAAAATT 36384 36385 TGATITITITICITCTICATITAAATATATCCATGGATTITIGITITITCATATAAGA 36444 36505 TIGIAAACTTACTTTAATTTTAATATGATTAATAAATTATAAGGGAGAATTTTTATGTA 36564 36565 TAAAAATGGTTTTTTAAAAACTATTTGTCATTGTTTTTAATTTTTTTAGTAATTGCTTG 36624 65 tatctgtttattatgatttcagggcgcaaaatgcgagtacttaataaaattttacattt 124 125 aaattagaattttttttttatcaataaatattaatttattagttttattagaaatattaatt 184 Borrelia burgdorferi polynucleotide sequence #2.

Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.

Borrelia burgdorferi. New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease Claim 1: Page 672-737: 1128pp; English. 185 agaaaattttgaatccccgatttctcctccttttcttcgctattcatcattttctaacca ö Length 110000; Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO (Borrelia Accession Score 58; DB 1; Le Pred. No. 0.14; 0; Mismatches 165; 500001 X20248 Locus 510000 610000 710000 810000 910000 210000 from 36625 TACTTCAAAGATAGCTCAAAT 36646 ВР atctgcaaaagattttacaaat 386 fragments X20249 standard; DNA; 116277 2.78; (HUMA-) HUMAN GENOME SCI INC (MEDI-) MEDIMMUNE INC. X20248 100001 Begin (first entry) Matches 157; Conservative US-053344. US-057483. of 10 Similarity 18-JUN-1998; U12764 ntinuation (6 of 10) Sequence split into WPI; 99-081217/07 ragment Name 22-JUL-1997; 22-JUL-1997; 03-SEP-1997; 20-JUN-1997; W09858943-A1 04-MAY-1999 30-DEC-1998 White OR; X20248_05
Continuation (
WP Sequence spr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18742 TCTCTTTCTGTTTTGAATTTGCTTATAAATTTTTTGTAACTTTCAGAAAATTTAAAATT 18683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18502 TAAAAATGGTTTTTTAAAAACTATTTGTCATTGTTTTTAATTTTTTAGTAATTGCTTG 18443
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the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of blosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 aaattagaattttttttatcaataaatattaatttattagttttattagaaatattaatt 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tatctgtttattatgatttcagggggggaaaatgcgagtacttaataaaatttacattt 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39250 T;
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 agaaaattttgaatccccgatttctcctccttttttttgctattcatcattttctaacca
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                                                                                                                                                                                                                                                                                                                     Length 116277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rt of native GLURP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-WAR-1989; US-218885.
3-MAR-1989; DK-06218.
(STAT-) Statens Seruminst.
Dzlegiel M. Borre M. Jepsen S, Vuust J, Rieneck K, Wind A,
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                             14490 G;
                                                                                                                                                                                                                                                                                                                                                      ed. No. 0.15;
Mismatches 165;
                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                             19868 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding carboxylic terminal par Plasmodium falciparum; antigen; malaria; Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                           Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                             42656 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18442 TACTTCAAAAGATAGCTCAAAT 18421
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                                                                                                                                                                                                                                                                                                                        2.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   003875 standard; DNA; 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 48.8
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2352
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                                                                                                                                                                                                                             116277 BP;
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P-PSDB; R05804
                                                                                                                                                                                            Lyme disease
Sequence 1
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DT 24-Aug
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DE 28-Aug
DE PLASMO
PH W09022
PR 03-WAR
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repeated tandemly 11 times. This last repetitious region consists of 360bp repeats differing only in 3 bases GAT coding for aspartate. This region is flanked to the 5' terminal of a degenerated 60 bp repeat. GC content of the conding part of the insert is on average 30%, and of the non-coding 3' terminal 11%.

Sequence 3095 BP; 1443 A; 300 C; 491 G; 861 T;
                                                                                                                                                                                                                                                                                                                                                                                                  2285 ITATICAAGIIGIAAGIACAAITAAAGGAAIAGCAAAGGATAIAGIAATATI--ITICCA 2342
                                                                                                                                                                                                                                                                                                   340
                                                                                                                                                                                           225 AGAAATTTAAAAAAGTATCTCAAACTATTGTAAGTGTTATGATTAATGCATATGATGGTG 2284
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                                                                                                               Length 3095;
                                                                                                             Score 57.2; DB 1; Length 3 Pred. No. 0.19; 0; Mismatches, 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-1990 (first entry)
Sequence encoding the SERA protein of Plasmodium.
Malaria, SERA protein; vaccine; ds.
Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2523 AATAAAATAAATAATTTCTTTCTTAGTTGT
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/label=Allele.II.
3092
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'note="Sequence
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note="Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q03568 standard; DNA; 6124 BP.
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7599.
                                                                                                              2.6%;
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                                                                                                              Query Match 2.6
Best Local Similarity 50.3
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
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722. .
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851.
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Plasmodium berghei ANKA strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding SERA antigen of Plasmodium falciparum - also DNA encoding signal and regulatory sequences of SERA gene, for diagnosis, prevention and treatment of malaria.

Disclosure; p; English.
Sequence allows for production of antigenic malarial proteins, useful in diagnosis, prevention and treatment of the disease. The sequence may be used in an expression vector; and signal and regulatory sequences may be used to stimulate production of other products.

Sequence 6124 BP: 2567 A; 602 C; 801 G; 2137 T; 17 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1064 ATAATTAAAAATGATTGGGGTAGTATTACCAACAATATTTTTTTATAAGAACCTTATCTAA 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     label-Complementary to Probe B. note-"Alelle II, skips 3098. 3136." 85. 2526
                                                                                                                                                                                                                                                                                                                                                                                 label-Complementary to Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label-Regulatory sequence
                                                                                                                                                                                                                                                                                                              *tag= r
note="Absent in allele
091. .3120
                                                                                                                                                                                                             *tag= p
label=Allele II.
                                                                                                       *tag= n
label=Allele II.
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098. .3136
*tag= l
label=Allele II
                                                                   label-Allele II
                                                                                                                                                                                                                                                                                                                                                                                                     note-"Alelle I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DART-) Dartmouth College.
Inselburg JW, Bzik DJ;
PPI; 90-083508/11.
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963 aaagattttttaaaaaaaagtataaaaattatattattcatgatttttcatacatttgatt 1022
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                                                                                                                                                                                                                                                                                                 1603 GAAATAAATACGACCTATTATAATCTTGTTATCTAAAAACTTTTTATATTGGAAGAAAAA 1603
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ttcatggtgttggtctgaggaggatttggcactatagaactctcctacggaccattctt
                                                                                                                                                                                                                                                                                                                                                                                                                     543 caaaacttcctacttacttcgtgcgttcggtaatcggtaacattagactttcaaaatcat
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Malaria: infection: therapy; diagnosis; vaccine; plastid;
PSI-PL470 gene; ds.
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V33135;
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AU-004953. AU-006329: AU-009481

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GBP 130 h and proteins produced
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Best Local Similarity 44.3
Matches 278; Conservative
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                                                                                                                                                                 Plasmodium is
                                                                                                                                                                                                                                                     (A) specific probes and primers (see V31139-56). The method is used to diagnose Plasmodium infection. Also (not claimed) the polypeptides encoded by (A) are useful as targets for drug. development and for development of anti-malaria vaccines. The high degree of similarity between (A) from different species allows development of genus- or species-specific assays that result in Sequence 5849 BP; 2296 A; 673 C; 557 G; 2323 T;
                                                                                                                                           gene of the solid modern control of the TRNAS, tribosomal proteins and RNA polymerase subunits, amongst others Plasmodium is detected in a human or animal sample by treating it, or derived nucleic acid, with a plasmodium extrachromosomal genetic element or derived nucleic acid (A) and detecting any hybridisation. (A) can include the PSI-PL470, PLH-PPH, PRB or PWO gene, the mitochondrial coxI gene, and nucleic acids derived from them. Also new are
                                                                                                                   is the nucleotide sequence of one strand of the PSI-PL470 of the 30.7 kb extrachromosomal plastid of Plasmodium berghei.
                                                                        extrachromosomal element - providing genus or species specific diagnosis with few false negatives, in humans or animals.
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 5849;
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                                                        Detecting Plasmodium infection from hybridisation with
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                              (ara AKU, Nelson JS, Tan TMC, Tham JM, Ting RCY;
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27-JAN-1992; 101271.
21-FEB-1991; DE-105348.
(BEHW ) BEHRINGWERKE AG.
Hundt E. Knapp B. Kupper H, Nolte D, Kuepper H;
WPI; 92-286009/35.
                                                                                                                                                                                                                                                                                                                                                                                                                2.6%; Score 56.4; DB 53.1%; Pred. No. 0.25;
(MOLE-) INST MOLECULAR & CELL BIOLOGY (UYSI-) UNIV SINGAPORE NAT.
                                                                                     diagnosis with few false negatives, i
Claim 15; Page 54-59; 120pp; English.
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Q27886/c
ID Q27886 standard; DNA; 2418 BP.
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P.falciparum GBP130h.
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vaccines to control malaria
Claim 1: Page 12-14: 17pp; German.
Glycophorin binding protein 130h is a P.falciparum blood stage
antigen 69% homologous with the known GBB130. The GBP130h gene and
its homologues can be used in vaccines to protect against malaria
caused by P.falciparum. The coding sequence was isolated using PCR
techniques on a genomic P.falciparum FCBR strain library. The
GBP130h gene was found to be highly conserved between different
strains but is distinct from the GBP130 gene.
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U11584 Drosophila

AL034556 Plasmodiu

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1 atcgatagagacatgttatt.....gtttttgaagtataaagatg 2165
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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				BASE	W Be	o, da	S S	. dg	o da o da	-
S	DMU11584 DMU11584 4601 bp DNA INV 23-JUL-1994 LOCUS DEFINITION Drosophila melanogaster Oregon-R mitochondrial A+T region. ACCESSION U11584 GI:508826 KEYWORDS mitochondrial DNA; A+T region; tandem repeats.	SOURCE fruit fly. ORGANISM Mitochondrion Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neotera; Endopterygota; Diptera; Brachycera; Miscomorpha; Ephydroidaa, Drosophila	REFERENCE 1 (bases 1 to 4601) AUTHORS Lewis,D.L., Farr,C.L., Farquhar,A.L. and Kaguni,L.S. TITLE Sequence, Organization and Evolution of the A+T Region of Drosophila melanogaster Mitochondrial DNA JOURNAL Mol. Biol. Evol. 11, 523-538 (1994)	MEDLINE 94285822 REFERENCE 2 (bases 1 to 4601) AUTHORS Kaguni, L., TITLE Direct Submission JOURNAL Submitted (28-JUN-1994) Laurie S. Kaguni Ph.D, Dept. of Blochemistry, Michigan State University, East Lansing, MI,	48824-1318, USA FEATURES Location/Qualifiers. Source 1, 4601 /organism="Drosophila melanogaster"		ene 1. 4601 /gene="mt:ori" /note="mticchondrial origin" /allele=""	/db_xref="FlyBase:FBgn0013687" repeat_unit 650. 1022 /gene="mt:ori" /note="repeat I-A"	/db_xref_FlyBase:FBgn0013687" /rpt_type=tandem repeat_unit 10231360 /gene="mt:ori" /note="repeat I.B1" /rbt_type=tandem	repeat_unit 1361. 1705

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                                                                               8604 ATAATTTAATATAAAATTTTTAAAAATTTCT--TAAATGTATTATTATAAAAAAAAA 2661
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taataacaaattttgtcgttttcatggtgttggtctgaggaggatttggcactatagaac 462
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Drosophila melanogaster complete mitochondrial genome.
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                                                                                                              523 atattcaagcatatccctttcaaaacttcctacttacttcgtgcgttcggtaatcggtaa
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lary, D.O., Goddard, J.M., Martin, S.C., Fauron, C.M.
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Clary, D.O., Wahleithner, J.A. and Wolstenholme, D.R.
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Drosophila melanogaster mitochondrial DNA, a novel organization and
Transfer RNA genes in Drosophila mitochondrial DNA: related 5' flanking sequences and comparisons to mammallan mitochondrial tRNA
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Satta,Y., Ishiwa,H. and Chigusa,S.I.
Analysis of nucleotide substitutions of mitochondrial DNAs
Drosophila melanogaster and its sibling species
MOI. Biol. Evol. 4 (6), 638-650 (1987)
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Satta,Y. and Takahata,N.
Evolution of Drosophila mitochondrial DNA and the history
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Lewis, D.L., Farr, C.L. and Kaguni, L.S.
Drosophila melanogaster mitochondrial DNA: completion of nucleotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)
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Michigan State University, East Lansing, MI 48824-1319,
Location/Qualifiers
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                                                                                   Nucleic Acids Res. 11 (8), 2411-2425 (1983)
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/product="tRNA-1le"
/db_xref="FlyBase:FBgn0013685"
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Ballard,J.W., Olsen,G.J., Falth,D.P.,
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Science 258 (5086), 1345-1348 (1992)
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/product="tRNA-Gln"
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VLGNIITILTYYOWWRDVSREGTYGGLHTYYYTIGLRWGMILFILSBYLFFYSFWAF
FHSSLSPAIELGASWPPMGIISFNPFQIPLLNTAILLASGYTVTWAHHSLMENNHSOT,
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                                                                                                                            /translation="MPQMAPISWLLFIIFSITFILFCSINYYSYMPNSPKSNELKNI
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Pred. No. 1e-06;
0; Mismatches 531;
      'codon_start=1 .
'db_xref="FlyBase:FBgn0013685"
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/transl_table=5
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/db_xref="GI:1166533"
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/db_xref="GI:1166534"
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VSTIGSTISLLGILFFFFIIWESLVSQRQVIYPIQLNSSIEWYQNTPPAEHSYSELP
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KLFHLNQLFSWFVNSKILKFTLFMNFLSLGGLPPFLGFLPKWLVIQQLTLCNQYFWLT
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HSWTVPALGVKVDGTPGRLNOTNFFINRPGLFYGQCSEICGANHSFMPIVIESVPVNY
                                                                                                                                                                                                                                                                                                                                                      .MMMSTLITLFFYLRICYSAFMMNYFENNWIMKMNMNSINYNMYMIMTFFSIFGLFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ranslation-"mSRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGDDQIYNVIVTAHAFIMIFFMVMPIMIGGFGNWLVPLMLGAPDMAFPRMNNMSFW
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/protein_id="AAC47813.1"
/db_xref="GI:1166532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="cytochrome c oxidase subunit
protein_id="AAC47812.2"
db_xref="G1:7412849"
                                                                                                                                                                                       'product - "NADH dehydrogenase subunit
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Control = TAAA stop codon is completed leadings to the mRNA*

Codon_start=1
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transl_table=5
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/gene="mt:ND6"
/product="tRNA-Trp"
/db_xref="TlyBase:FBgn0013685"
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/transl_table=5
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//gene="mt:ND6"
/product="tRNA-Lys"
/db_xref="flybase:FBgn0013685"
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/gene="mt:ND6"
/product="tRNA-Asp"
/db_xref="FlyBase:FBgn0013685"
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/db_xref="G1:1166530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1322, 1383)
/product="tRNA-Cys"
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/product="tRNA-Leu"
                                           'product="tRNA-Phe"
                     'gene-"mt:ND6"
                                                                                                       e-mt:ND6
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/gene="mt:ND6"

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                                                                                                                                                        Squares, R., Squares, S.;
, Newbold, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - tttcttaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaag 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holodium falciparum MAL3P5, complete sequence.

AL034556 AL0008971 AL0008972 AL0008978 AL010141 AL010153 AL010162

AL010206 AL010210 AL139179

AL034556.2 GI:4493931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete nucleotide sequence of chromosome 3 of Plasmodium
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 86829)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowman, S., Skelton, J., Churcher, C., Lawson, D., Quail, M. and
583 cattagactttcaaaatcatttttaacccctaaacagtaaatttgaaggacaaaaataat
                                  atttttcaaatttgatagactattttttttttgtaatttgacgaaccaaaaccagattta
                                                                                                                                                                                                                 taaaacaaaatttcatggcagcatgcctcagcccatgaaaaaaaccttataaaaatatct
                                                                                                                                                                                                                                                                                                                                                                                                                              tatttttaagatattaattaagaaattaaagatt--ttttaaaaaaatgtataaaatta
                                                                                                                                                                                                                                                                                                                                                       875 acataacatggatatctccttaccaatcatactaattattttgggttaaatattaatcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acacattgaccattgaaaagttcgttctcccatgggtaaccagatcaaactcacatccaa
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Sulston, J. E., Whitehead, S., Woodward, J.R.,
Barrell, B.G.
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rect Submission
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The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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FIKKNI DNNI SNDI SNNE I NI I KLKKLNQSDED I NLTSDLIY ERLRTKYLMY I OK I EY
LKFKYQYDI I NEQYPI I KNEKTYLDLLNYGY KI VMSPDVDNSLFEKTKI DSI PNEKDK
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                                CB10 1SA, UK On Mar 24, 1999 this sequence version replaced gi:4034877. On Mar 24, 1999 this sequence or the Malaria Project, see http://www.sanger.ac.uk/Prójects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="predicted using hexExon; MAL3P5.1 (PFC0575w),
Hypothetical protein, len: 645 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted using hexExon; MAL3P5.4 (PFC0590c),
Hypothetical protein, len: 1828 aa"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted using hexExon; MAL3P5.2 (PFC0580c),
Hypothetical protein, len: 1097 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(324. .668,1199. .1303,1460. .2944)
gene="MAL3P5.1"
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                                                                                                                                                                                                                                            organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xref="SPTREMBL:097258'
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/db_xref="G1:4493932"
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/db_xref="GI:4493950"
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                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:5833"
/chromosome="3"
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                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="MAL3P5.1"
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                                                                                                                                                                                                                                                                             /strain="3D7
                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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SFOHYIKKLKTCRFDADDIRNLLEKRLAYERDNTLIKNIOEEENKKGIGINGNFGSES
NSSSSNYDNNYLLYRKINRLNKTNTNKSKNRSRKRRRINSKIDKKYIIKCRACKFINP
                                                                                                                                                                                              TKLLISILKKRRNGPLPFLQKCYIHNVPRINTMKHMNISDLRKNIEVCNKKNVKHKNV
WSNFLYIIILKLFNKEIKNYVDFMIILKLLSKYIKIEKKVLLYICEQIEHEIYKFRTR
                                                      NIDY I ENNI IYSY IKSFKRTPPITKI YLLGTFLLSVLIHMNKNVYKLILFDFNKI FKK
GEIWRLFTPYLY IGNLYLQY ILMFNYLNIYMSSVEI SHYKKPEDFLI FLTFGY ISNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIQLKKKKINKINNNNNNNNNNNIYIDTNIQTVNKNYSCTHNNVIKNETNDNYPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLFPKNITLLRGNHESRQITTVYGFYDECFKKYGNANAWKYCTDIFDYLTLAALVDNQ
IFCVHGGLSPEIKLIDQLRLINRVQEIPHEGAFGDIMWSDPDEVDDWVANPRGAGWLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPNVTKKFNHINNLELIARAHOLAMEGYRYMFEDSTIITVWSAPNYCYRCGNVAAIMR
IDEYMNROMLIFKDTPDSRNSIKNKATIPYFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation-"MKKYLNKYMYIYNIYNKLEEKYKNFLKLKNMNSHMGASQNMNVN
                                                                                                            FTIMANMYNENIMNVKLYIHNFKNFFIKDCVSKYTSRSSTNNNSNNINSNNRSSNNNN
HYNNSKNIDIKKEQYNHLGYVFSTYILYYWSRINEGTLINCFELFFIKAEYVPFFFII
                                                                                                                                                                                                                                                                                                                                                                                                                                      I NI YVNI NKI YLNDEEENTSHCI LKI KNDNKKDI LYHDHMKFLYNLMNEI I YRNDLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLYIHDDLFYMNKNKKRDRYKIYLYDNFIFNYPAYYVEQKKDHIDYNESVNNFDNMKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIRNOHPNDQVILNNPVFFYNKKLNVVDSIDFEYELTCYNLYLDIYKIVCKKLLTLKK
NHKLSCLQSIDILCIYEKLNIRDYRIIKYLYNLKKELLYLDNTYLLKVINIIVKFNLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THTNNLNKNEQHKYIHHNNDHKDGRHNNNNNHYDKVDVSSSSSSYYYYLNKSGKNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLIKVDKKKFLIVDILYNYDYYYTLTKSKLDKLKEYNIYLSYYSNHIKKKNKKILNYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation-"MAKGEERKWIEQLRMNPPKLLDESDLRLVCQRVKEILVEENNVQ
                                                                                                                                                                                                                                                       DLTLLILILKKUNFDNIYYINLISKSILMKMNKNMAMKDLALIIYSLSKNIYLTDEQI
YNKEIFNFSILKFENHLNNVNINLHSLSLFFYSYSVYFINNCFYYYYYFHSFFNIITK
                                                                                                                                                                                                                                                                                                                                                 IYLKNINNNCYDHRLDSNDFITMINYDQGEYNKHIQQNKHIQQNKHIQQNKHIQQNKH
                                                                                                                                                                                                                                                                                                                                                                             IORIGTHCTESNSNNOOLIQIONDEKENKLITYDNSKHNLLKDPCOHNIVEKDGEKKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKQ I ILLLYGLKFNNFMFLQFEK I ILKRF I CLPKKE I QK I GKEEIMFLYQY FFVRTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNELKKONNLFISODEYENYIYISDKYNESAKLDNSYNMPSNLKEKNTNHHGGKDNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFKNLYNLONIODLKK I EMMNVYDNLTFKFYKLFKNI LS I NVKRYVONCNSYNKY EMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYALLKLIKKRGFNYICIDADTYVKNKKGKSKDLSYEINKLYINNLILDILKRQKKNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIKNINIKNKLLLYHQNKKNVKKIIHFKNYKYKIMNLPDQRNHYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMISYLQINKILTFINYNNINESIQILKLIGMLISVHKHNKLSPFHMNNLNVQNAANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine/threonine protein phosphatase (PP2), len: 309 aa Similarity to serine/threonine protein phophatases. M. domestica serine/threonine protein phophatases. (TR:042912) BLAST Score: 1005, sum P(1) = 6.9e-107; 60% identity in 301 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MAL3P5.7"
/note="predicted using hexExon; MAL3P5.7 (PFC0605c),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="predicted using hexExon; MAL3P5.6 (PFC0600w),
Hypothetical protein, len: 250 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKRIKY IKDKSLLAINHKTKNIIEKOKISTSNHLSKLKRMFSL'
RYGGIYNSKYMTIEKRRKYNYIKKQKNNNNSYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .26157)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="MAL3P5.5"
/note="predicted using hexExon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGFKIEDYYTCQNCGYNDFSVIRSTSPNNAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xref-"SPTREMBL:097259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Join(25252. .25296,25453.
/gene="MAL3P5.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'protein_id="CAB38970.1"
'db_xref="G1:4493934"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25252. .26157
/gene="MAL3P5.6"
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/translation="mahkvkkekkteaqetpvvakeqthakeennesniavteenvis
kngqeiaiskndqeiaiskndqeiaisnndqeiaiskndqenvalnsseerqnaskee
Dnelkqikefhdisnenehnenrsfststlssffkeyeensveqhffsegthtehsme
                                                                                                                                                        KKDEFESTISTLKKNMTKNEDSDNNTNNFYDENGEKKTTTNYCNDHINLFIDEEKELT
AKOKKHEEFLIKKGHY1YYDKNFNTQHNSIYDKNKNAQIISDFNKMKLCERDWFLNKK
NKNEKTKDNGANFFHIQKDNISEEHNKTENINSDLSLYCNTNNYITHDKKKEKKQMHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSNNVETIENAITNDVLRSNRSTSYSKOKNELTSVTCYVCGETVDLNIWSDHIFAHKL
                                                                                                                                       /translation-"MGGHGGLNILPQKKWNVYRKDAQYKVHYDEHKIIKEEKDKEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATATTATTTAATTTAATTATTATTTTAATATATATATTAAGTGGAATAAAATAAAATT 39799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTIATITITATITATIAATATATITATIATATAACIGCTIATITAATICATITAATIAA. 39739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATATATTATATTAATTTGAATTATTAATTTATTATAAAATTTAATTAAAAA 39679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttttcatggtgtttggtctgaggaggatttggcactatagaactctcctacggaccattct 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 aaccaatcttat -- - atgttcttcaaattagaacttgaaattattaattataattaaac 300
                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using hexExon; MAL3P5.8 (PFC0610c), Hypothetical protein, len: 1182 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 atagagacatgttattcacaaaccataaaatgatggctaaaattggtgtgttgattggaacga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatotgtttattatgatttcagggcgcaaaaatgcgagtacttaataaaattttacattt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aaattagaattttttttttatcaataaatattaatttattagttttattagaaatattaatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 86829;
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  aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99.8; DB 33;
Pred. No. 0.00013;
0; Mismatches 617;
248
                                                                                                                                                                                                                                      HIKKIIKYKQEKDKEKKRKRGGKEKKKPK"
complement(29992' .33537)
                                                                                                       /db_xref-"SPTREMBL:09Y011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"SPTREMBL:097260"
                                                                                                                                                                                                                                                                                                                    complement(29992. .33537)
/gene="MAL3P5.8"
                                              /protein_id="CAB41709.1"
/db_xref="GI:4725991"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB38971.1"
/db_xref="G1:4493935"
                                                                                                                                                                                                                                                                                                   /gene="MAL3P5.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
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llarity 45.4%;
Conservative
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Matches 529; Conserv
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RYGGI YNSKYMT I EK RRKY NY I KKQKNNNNSY FSYCNVYKNNDVNNYTAYNY I INNP
KNKLKEY Y EK I KNHV I KKKKKI FSLKFSQNKRNEKKKKYPFI NFTSFHD I KDNIKVLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I EOAD I EFONFLSNYNLDOHGRYKSNDENTKSTEH I KNKNT I NKGYDTEL I QNGMENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIKKNIDNNISNDISNNEINIIKLKKLNOSDEDINLTSDLIYERLRTKVLWIOKIEY
LKFKYQYDIINEQYPIIKNEKTVLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'NIY INFYMINILKY ICYKNMEI ILLNYNH I EDMKKK I NQKNNTNTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKKKKKKKKNPKVHSILNOISEKVKEKKDAENYLALHLFLLKDENITLFSMMHIMDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LY FNY HY DELL RCFTMKLNI ERNNKNI I RSNY DNI NNDI SI DK DMY MNNPI DVNI NNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ?YDHINSSSNRCSFKNLKKOOTDDNTKHIIMGKEKYPMNKSDHEKKNNNTCGNINIEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELAKIYTNNIFDYLKGKKEKHQNEDNTINLYYIKKKFPWIFYLKNIIKNKDTSFIEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"predicted using hexExon; MAL3P5.2 (PFC0580c), Hypothetical protein, len: 1097 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="predicted using hexExon: MAL3P5.4 (PFC0590c), Hypothetical protein, len: 1828 aa"
                                                                                                                                                                                                                                                                                                                                             /note="predicted using hexExon; MAL3P5.1 (PFC0575w),
Hypothetical protein, len: 645 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSPOIYRKRFKRSRIKNVSFKKKOKKPLFLFENLKKGFSFLGFWRNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(13655, .17801,18019, .19355))
/gene="MAL3P5.4"
see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                            324. .2944
Join(324. .668,1199. .1303,1460. .2944)
/gene="MAL3P5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYTQRIQNCCDIFSYIYKKYNFNEKNPFLNYLYY
                                                                                   /organism-"Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref-"SPTREMBL:097258"
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/db_xref="G1:4493950"
                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB38969.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="CAB38968.1"
db_xref="GI:4493932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6646)
                                                                                                                 /strain="3D7"
/db_xref="taxon:5833'
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                                                                                                                                                                                                       /clone="MAL3P5"
324. .2944
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                                                                                                                                                                               /chromosome="3
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                                FEATURES
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Lawson,D.

Bowman,S., Lawson,D.

Churcher,C.M., Craig,A., Davies,R.M. Devlin,K., Feltwell,T.,

Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S.,

Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J.,

Moule,S., Mungall,K., Murph,L., Oliver,K., Quail,M.A.,

Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S.,

Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and
                                                                                                                                                                                                                                                                                          39271 TTAATTTATTTTATTTAATAATAATATATTAATTTAATTTATTTATTTATTTAATTAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39093 TATATATAACTATTACATATATTTTTTTTTTTTTTAATATATTTATAAATATTTTATTATTT 39034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mar 24, 1999 this sequence version replaced gi:4034877.
more information about this sequence or the Malaria Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               taaaagattttttaaaaaaatgtataaaaattatatatteatgattttteatacatttga 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttttgataataatatatttttttttaatttcttaaaaaatgttgcaagacacttattaga 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081 catagtottgttotgtttacaaaagcattcatcatttaatacattaaaaaatatttaata 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum MAL3P5, complete sequence.
AL034556 AL008971 AL0008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179
AL034556.2 GI:4493931
        661 actatttttttttttgtaatttgacgaaccaaaaccagatttatcctgaattttaggaacc 720
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                                                                                                                       721 acagatgtaactaaaccaatatttattttattttctaaaacaaaatttcatggcagcatgc
                                                                                                                                                                                                                                        781 ctdagcccatgaaaaaaaccttataaaaatatctacaccattgaccattgaaaagttcgtt
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us-09-464-528-14.rge

ONILLYNEFSLYEVASIFSSYLEFTYERYFKENYLRLFFKTLLKVIHIYPLYDRFOMN
TKLLISILKKRKNGPLPFLOKCYIHNVPRINTMKHMISDLRKNIEVCNKKNVKHKNV
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FINIINKNLHLYNSTDLMFLYIGSLHIHNMYTPNHYDONKEPKNNYKHNDNHN FNELKKONNLFISODEY ENTITISDKYNESAKLDNSYMMENELHTELLITITISTER FNELKKONNLFISODEY STATEL BETTELLITITISTER FNELKKONNLFISODEY STATEL BETTELLITITISTER FNELKKENTYHHGGKEDTL BETTELLITITISTER FNEKTHNYTHREGNENTSTATEL BETTELLITISTER SYNNEDNENTSTATEL STATEL BETTELLITISTER FNEKTHNYTH SYNNEDNENTSTATEL SYNNEDNENTSTATEL BETTELLITISTER FNEKTHNYTH SYNNENTSTATEL SYNNED SYNDENTSTATEL SYNNED SYNDENTSTATEL SYNDENTSTATEN SYNDENTSTATEN SYNDENTSTATEN SYNDENTSTATEN SYNDES SYNDEN SY LFKNLYNLQNIQDLKKIEMMNYDNLTFRFYKLFKNILSINVRRYVQNCNSYNKYEMN
THTNNLNKRECHKYTHHNUDHKDGRHNNNHYTDKUDVSSSSSSYYYTLNKSGKNLG
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KLIKVDKKKFLIVDILYNYDYYTLTKSKLDKLKYNIYLSYYSNHIKKKNKKLLNYK /translation="Wkkylnkymylyniynkleekyknplklknmnshmgasonmnvn npythmeleeperinnnynnninninnynynynynsosoyohmeklodpynnkn spythmeleeperinnnynninninnynynynynyn spohylkklætorpoaddirleeria/bednylikniobedenkojiginonposes nssssnydnnyllyrkinrlinrlinkynnskrrrinskidkkylikcrackfinp FTIWANMYNENIMNVKLYIHNFKNPFIKDCVSKYTSRSSTNNNSNNINSNNRSSNNNN IORIGTHCTESNSNNQQLIQIQNDEKENKLITYDN<mark>Y</mark>KHNLLKDPCQHNIVEKDCEKKQ NLIKNLIINIKKIIEEKLSSFKIQEIVNILFVSLNKNIIINKKYFHFLNQEKINIRNY INIYVNINKIYLNDEEENTSHCILKIKNDNKKDILYHDHMKFLYNLMNEIIYRNDLLN MKQIILLLYGLKFNNFWFLQFEKIILKRFICLPKKEIOKIGKEEIMFLYQYFFVRTCL KYALLKLIKKRGFNYICIDADTYVKNKKGKSKDLSYEINKLYINLILDILKROKKNH LHPHPHTONRTTKOIKNINIKNKLLLYHONKKNYKKIIHFKNYKYKIMNLPDQRNHYH NKRIKYIKDKSLLAINHKTKNIIEKOKISTSNHLSKLKRMFSL" HYNNSKNIDIKKEOYNHLGYVFSTYILYYWSRINEGTLINCFELFFIKAEYVPFFFII IYLKNINNNCYDHRLDSNDFITMTNYDQGEYNKHIQQNKHIQQNKHIQQNKHIQQNKH /db_xref="SPTREMBL:097259" /translation="MAKGEERKWIEQLRMNPPKLLDESDLRLVCQRVKEILVEENNVO LLFPKNITLLRGNHESRQITTVYGFYDECFKKYGNANAWKYCTDIFDYLTLAALVDNQ TYCWGGESPERLIDOLLTHRNQEIPHEGAFGDIMMSDPDEVDDWYANPRGAGWLF GPNVTKFKHIINNLELARAHGLAMGSYXMFEDSTIITVWSAPNYCYRCGNVAAIMR IDEYMNRQMLIFKDTPDSRNSIKNKATIPYFL" SIKPPVIICGDIHGQFFDLLELFDVGGDIMNNDYIFLGDYVDRGYNSVETFEYLLLK Serine/threonine protein phosphatase (PP2), len: 309 aa. Similarity to serine/threonine protein phosphatase. M.domestica serine/threonine protein phosphatases. M.domestica serine/threonine protein phosphatase. (TR:042912) BLAST Score: 1005, sum P(1) = 6.9e-107; 60% identity in 301 aa overlap." /note="predicted using hexExon; MAL3P5.6 (PFC0600w), Hypothetical protein, len: 250 aa" /note*"predicted using hexExon; MAL3P5.7 (PFC0605c). Hypothetical protein, len: 248 aa" gene="MAL3P5.6" |Oin(25252. .25296,25453. .26157) |gene="MAL3P5.6" /gene="MAL3P5.5" /note="predicted using hexExon; NGFKIEDYYTCQNCGYNDFSVIRSTSPNNAD' /db_xref="SPTREMBL:097261" /gene="MAL3P5.5" complement(20528. .21454) complement(20528. .21454) 'protein_id="CAB38970.1" 'protein_id-"CAB38972.1" /protein_id="CAB41709.1" /db_xref="GI:4725991" /db_xref="GI:4493934" db_xref="GI:4493936" 'gene="MAL3P5.7" gene-"MAL3P5.7" /codon_start=1 /codon_start=1

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DNELKQIKEFHDISNENEHNENRSFSTSTLSSFFKEYEENSVEQHFFSEGTHTEHSME
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Hypothetical protein, len: 1182 aa'
                                                                                                                                                                                                                                                                                                                                                                                                       Score 98.4; DB 33;
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); Mismatches 581;
                                                                                               HIKKIIKYKQEKDKEKKRKRQGKEKKKPK"
                                                                                                                                                                                                                                                                                       /db_xref-"SPTREMBL:097260"
                                                                                                                               /gene="MAL3P5.8"
complement(29992. .33537)
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                                                                                                                                                                                                                                                 /protein_id="CAB38971.1"
/db_xref="GI:4493935"
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SSIFSKKRDSHKKGSSFRGRRSGFINRKSGSFKKPYYNNRLINKNYNNYKGRNFHNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koonin, E. V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J., Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D. C., Pertea, M., Salzberg, S., Zhou, L., Sutron, G.G., Clayton, R., White, O., Smtth, H.O., Fraser, C. M., Adams, M. D., Venter, J. C. and Hoffman, S. L., Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                Submitted (02-NOV-1998) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
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Plasmodium falciparum chromosome 2, section 35 of 73 of the
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1 (bases 1 to 14867)
ctcagcccatgaaaaaaaccttataaaaatatctacacattgaccattgaaaagttcgtt
                                                                                                          ctcccatgggtaaccagatcaaactcacatccaaacataacatggatatctccttaccaa
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/db_xref="taxon:5833"
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/protein_id="AAC71887.1"
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/gene="PFB0490c"
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/gene="PFB0490c"
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DNFKGRTGSFGSRVFDNRKGSFKKRFISNRNKSSVKSYRGNGSNKMGRKSFNKAPTSR
TVVTKRLNNYKTVSAPVKKFNNLNISLYRKNRTFALNTKRSKPVGTIKSSVPRKRIKK
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Pred. No. 0.00045;
0; Mismatches 531;
                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="AAC71888.1"
                                                                                                                                                                                                                  by GlimmerM"
                                                                                                         11241. .14606
/gene="PFB0495w"
11241. .14606
/gene="PFB0495w"
                                                                                                                                                                                                                     /note="predicted
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Best Local Similarity 46.8%;
Matches 483; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens BAC clone CTA-281G5 from 7p15-p21, complete sequence.
AC005083.
GI:4150930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jan 12, 1999 this sequence version replaced gi:3212908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
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                                                     ttcaaatttgatagactattttttttttgtaatttgacgaaccaaaaccagatttatcct
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1 (bases 1 to 146285)
Madsen,C. and Blair,T.
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University, 4444 Forest
4 (bases 1 to 146285)
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send
                                                                                                                                                                                                                                   this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                   NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nttp://www.nngri.nin.gov/bix/Gib/Chk/ , senu
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to 12345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone CTA-281G5 is from a release of the human BAC library CITB-HS-A. The library contains cloned DNA from human sperm. Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics 34:213-8 (1996). The clone is available Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of CTA-281G5;
actual end is at 146285 of CTA-281G5
Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC CTA-281G5 contains an E. coli transposon from 10982 that is not represented in the submitted sequence. Location/Qualifiers
                                                     /rpt_family="purine-rich"
6891, .7126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            confirmed by restriction digest.
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/rpt_family="AT_rich"
1264. .1720
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5764. .6034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="7'
                                code: WUGSC
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7. .10477
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/rpt_family="AT_rich"
'504. 7554
'rpt_family="AT_rich"
320. 8348
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59. .11049
                                                                                                                                                                                                                           family-"AT_rich"
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11461 ATTAATATGATATATATGTAATATATTATTCATATATATGATATATGATATGTAATAT 11402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  attagaaatattaattagaaaattttgaatccccgatttctcctccttttcttcgctatt 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 gataattaattgataaatctgcaaaagattttacaaatatctttcagaaaaaattaataa 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 aagcatatccctttcaaaacttcctacttacttcgtgcgttcggtaatcggtaacattag
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 146285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.6; DB 39;
Pred. No. 0.00089;
0; Mismatches 569;
                                                                                                                                                                                                                                                                                                                                                                          38324. .38899
/rpt_family="Retroviral"
                                                                                                                                                                                                                                              61. .35288
t_family="(CATTT)n'
                                                                                                                                                                                                                 t_family="AT_rich"
                                                                                                                                                                                                                                                                                         t_family="(CA)n"
                                                                                                                                                      "MIR"
                                                                                                                                                                      36. .32730
t_family="MIR"
                                         /rpt_family="Alu"
30744. .30982
                                                                       'rpt_family="MIR"
1032, .31739
                                                                                                           rpt_family="L1"
2332. 32449
                                                                                                                                                                                                                                                                                                         1. .36007
family="L2"
                                                                                                                                                                                                                                                                                                                                               /rpt_family="L1"
38324. 3000
                                                                                                                                               rpt_family='2536. 32720
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 44.5%;
Matches 467; Conservative
          rpt_family:
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//gene="MALIP3.01"

complement(join(1748. .2598,2748. .2848,2990. .3276))

//gene="MALIP3.01"

//note="MALIP3.01"

//note
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The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Dec 16, 1999 this sequence version replaced gi:5763807.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="conserved hypothetical protein, UPF0006 family"
/protein_id="CAB63556.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M. and Barrell,B.
                                                                                                                                                        attiticatacatitigatititigataataaatatatititititaatiticitaaaaaaaggit 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcaagacacttattagacatagtcttgttctgtttacaaaagcattcatcatttaataca 1123
                                                                                                                                                                                                                                                                                                                                                                                                              gatattaattaagaaattaaaaagattttttaaaaaatgtataaaaattatattcatg 1003
                                                                                                                                                                                                                                                 totoottaccaatcatactaattattt----tgggttaaatattaatcattattttaa 943
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1 (bases 1 to 67970)
                                                                                    gaaaagttcgttctcccatgggtaaccagatcaaactcacatccaaacataacatggata
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Plasmodium falciparum MALIP3, complete sequence.
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/strain="3D7"
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Plasmodium falciparum
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PFMAL1P3
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IVNIKRLNNY INDH

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/translation="MKLLNNRFVVLCPIIILFFLNSVVLGNNNRNNINFHETENAAK
AMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEBEKYSGTDLFR
KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
                                                                                      LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
CSLKSLENINAVKKIPLNLLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
I LITCTCLAEIDKSLKICETYDPEGKFLYLSAGVHPTNCYEFIDKNKHEEKE
                         I I A K K E Y E E F I K Y F K N E Q V E N S K M E N G N K I C D G E K D M N L N E I L E K N L D T I P G F K Y
                                                            NEKDKEY LEULKNK I I KY PNR I VCIGE IGLDFDRLY FCSKY IQIKY FI FQLKLVQMFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note-"possible cen1, region of very high [A+T] content" (4884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="MAL1P3.03, putative ABC transporter, len: 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MAL1P3.02, hypothetical protein, len: 163 aa, contains possible signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="potential splice donor sequence, aaa/gtaaaa"
                                                                                                                                                                                                                                                                                                                               /note="potential splice donor sequence, atg/gttaaa"
complement(2849. .2861)
/gene="MALIP3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="hypothetical protein, MALIP3.02"
protein_id="CAB63557.1"
lb_xref="G1:6594245"
                                                                                                                                                                                                                               /note="potential splice acceptor sequence" complement(2742, 2747) /gene="MALIP3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                  acceptor sequence"
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protein_id="CAB63558.1"
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="potential splice
complement(2984, .2989),
/gene="MALIP3.01"
                                                                                                                                                                            complement(2599, .2610)
/gene="MAL1P3,01"
                                                                                                                                                      IIKCDDNTIFKERNEPYNIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Juus. .5496
/gene="MALIP3.02"
5005. 5406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4884. .20352
gene-"MAL1P3.03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement
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rRNA

gene gene

CDS

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/translation="mrikmnsgiffiklldisficvfecfnkcmisyrkdllmysen
Cfnysidrslaegssesketkvkdipniellkslninyeeyekmkeivgsfmdnnnln
Ianevlknihsftnienifslindsskspvlktfikefgsifphmlnnvpkllfdlco
KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISOG
KITVEGRDIRTYNRKGEDSIIGILAGSSFVFYNMNIRTFIDPYNNFTDEIVHALKLN
GINLGKNDLYKYMHKODMKSNKKIIOTSKVINQSNDWIILLTNDCIRYLSLVRLYLN
RHKYRIILIDEIPIPRANNYHDELMSFLIGKAKSFRYIIRNHFPNNTVLIISHHANT
LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="WKKSYTFINVTILLFLTYYNYDFSKTKFNNNIKIDIN
RFKRIIAEASEEQKYPWEEDFCLILNEEELIRPEHNDSPYLPEHYENIDKINELSINS
TKIWKETIKKKRQNYEKETDKMNHNRDFWHHYKWANIYLYKHKLINITLKDLTNPI
HDKETITTWIKMIQDEDIEYFLFNLQVEWLRILTLELFYKNKE"
complement(32477. 32486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MALIP3.04, conserved hypothetical membrane protein, len: 203 aa, similarity: P. falciparum chromosome 2, PFB0110W, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity in 191 aa overlap)"
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Itgrilneteleknkodnsksetlikeekdekddvpttsnoniknahnnneissstop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNI INVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKDKKEKHKKEKKHKK
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KIEKKKKKQEEVEKKKQEKERKKQEKKERKQKEKEMKKOKKIEKERKKKEEKEKKKKK
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EHKEEEEHKEEEHKKEEHKS KEHKSKGKKDKGKKDKGKHKKAKKEKVKKHVVKNV I EDE
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fasta scores: 97.6%
                                                                                                                                                                                                                    /note="region containing small subunit, 5.8S and large subunit rRNA genes and spacer regions" 23896. .31533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aa.
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complement(32669. .32674)
/gene-"MALIP3.04"
/note-"potential splice donor sequence, aaa/gtatat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roduct = "conserved hypothetical membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(3657. 36743,36864. 37343)
/gene="MALIP3.05"
/note="MALIP3.05, hypothetical protein, len: 188
                                                                                                                                                                                                                                                                                                                                                                          /gene="MAL1P3.04"
complement(join(31966. .32476,32675. .32775))
/gene="MAL1P3.04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="hypothetical protein, MALIP3.05"
protein_id="CAB63560.1"
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/protein_id="CAB63561.1"
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Identical to GARP_PLAFF (678
Identity in 678 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNPLHILGLIVILAAIYVFENFKNFEC
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                                                                                          /note="potential splice donor sequence, aag/gtaaca"
                              DODAEEDDODAEEDDODEDEDEEEEEEEEEEESEKKIKRNLKNAKI"
                                                                                                                                                                                        272 gaacttgaaattattaattataattaaactgaaaacaatttggtatcaattcatatacat
                                                                                                                                                                                                                                                                                                                                                                                                             9165 ITAAATTATTTAATATATAAAATAAATATATACGCTAATAAAATATTAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 attaatttattagttttattagaaatattaattagaaaattttgaatccccgatttctcc
                                                                                                                                                                                                                                                                                  tcagaaaaaattaataacaaattttgtcgttttcatggtgttggtctgaggaggatttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                  452 cactatagaacteteetaeggaecattetttgeaetteaaetaaaegatggteagaattg
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                                                                                                                                                                                                                                                                                                                                                 332 gottagtaataaaatgcgataattaattgataaatctgcaaaagattttacaaatatott
                                                                                                                                                                                                                                                                                                                                                                     Length 67970;
                                                          //note="potential splice acceptor sequence"
complement(40204 .40209)
/gene="garp"
                                                                                                                                                        Indels
                                                                                                                                    DB 33;
                                                                                                                                                       547;
                                                                                                                                               Pred. No. 0.0014;
                                                                                                                                                        0; Mismatches
                                                                                                                                    Score 91.8;
                                         complement(39996. .40005)
                                                                                                    45401. .50233
/gene="MAL1P3.07"
                                                    /gene="garp"
                                                                                                                                     4.28;
                                                                                                                                               46.38;
                                                                                                                                                        Conservative
                                                                                                                                                Similarity
                                          misc_feature
                                                                      misc_feature
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Matches 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENARYOLE A. Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 153098)
Churcher.C., Bowman,S., Lawson,D., Quall,M. and Barrell,B.
Unpublished
2 (bases 1 to 153098)
Lawson,D., Bowman,S. and Barrell,B.
Direct Submission
Submitted (17-DEC-1998) P. falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation-"MNDNESLDSEVLEKQYEIIKYAKYQDFIRLQILIQPYLLNNDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLNSINILHWACYCGFTELVKKLISFNCDIEKEDLVNNDTPIYYAIKNSNYEIVLLLI
KCFGISILFHKNRRRMSPFLTAICEFNEDKILEALHILELLYMNGVSLEEQNEHGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLIVYFNIAHSFSIINKYHFKSLIWITIWFFQQFLWCMLYFKSPGFYKENHMFNKNKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Mar 24, 1999 this sequence version replaced gi:4034874. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is not the entire insert of clone MAL3P2. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
                                             1052 ttaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattca 1111
                                                                                                                                                                                                                                           Plasmodium falciparum MAL3P2, complete sequence.
AL034558 AL008982 AL008989 AL009007 AL009008 AL009009 AL009014
AL010140 AL010150 AL010158 AL010111 AL022217 Z97350 Z98546
AL034558.2 GI:4493878
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                                                                                                                                           HIYIYIYIFFFFFENEYLCDLQYYKTSKGSSLC
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1. .153098
/organism="Plasmodium falciparum"
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/gene="PFC0165w"
join(5344. .12004,12737, .13329)
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                                                                                                                                                                                                                                                                                             1112 tcatttaatacattaaaaaatatttaatact 1142
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Plasmodium falciparum
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gene="PFC0160w"
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gene="PFC0160w"
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PFMAL3P2/c
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EYKUNLNKVGDYFNKVNISLEDLELYYNNVVKNEYSNNINNNDMDIIEEVSLKCIKLA
MCKSMNESLQVPLFHLNEMCIINNLIKMRKEYKEQQKNLQTKETNITITCILIKLISN
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SLRDKANNMQLDKSDITNGTITVSNFGAISGTFATPIVFDNQACIIGIGKMEKKLLLK
                                                                                                                                                                                                                                                                            /translation="MNREKLIKLLEKENKNRMNIKNVKFRDCHCMFNNYSQCYVNVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYY KLVLIKKMTLKHLFUNOTDINILFSFHNACLSNY NKLDENY SYLLINNY NLNNNKS
EHLINISRKKNYTLDHTNNTY NNSNTNIITKNY SNNNHNNNNDNNILSNDLY SY FNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOKKKNEKRKKKSYKNIYDHSKENNRKOSNSIYSISSFSOKNYKNTNMINMNLHGEE
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/note="predicted using hexExon: MAL3P2.2 (PFC0165w),
Hypothetical protein, len: 1676 aa"
/codon_start=1
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lipoamide acyltransferases. C.elegans lipoamide
acyltransferase (WP.2K669.4) BLAST Score: 582, sum
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                                                                                                                                                                                                                                      /db_xref-"SPTREMBL:097225"
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/protein_id="CAB38991.1"
/db_xref="GI:4493882"
                                                                                                                                        /protein_id="CAB38989.1"
/db_xref="G1:4493880"
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/gene="PFC0175w" 17040. .18821

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Query Match
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HHNNNNIPSNVNFKSFHDNYITHNKINNNMPYENNTYLKNNYSVNIPQTYTTKEFANN
                                                                                                                                                                                                                              /db_xref="Sptrembl:097226"
/db_xref="Sptrembl:097226"
/translation="NNIPKEONKNOJINVTIEYGEOKKMVIKTPINDTKKNNIINHN
YDYSNINDKYKNTSDCYLMNNEDGINLYLNYYKKM*LKFQENNLYNYELKOIEKKME
LAILEIMNLINIOYDAYAHFELKAYRENSNDLLENMPRNSKKYLTKLKLSHLKEBDILN
NNNNNIDEPMIKOKKEQFVHNCKQEKFICPILFLECDIEDTYTLSCGHKYSKECLKN
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ILNRYNHFKSRFNDHOYAENFSIHTQLLFLYNFCKNYNIHLHKMKFFEDAIIQIIKCR
KILKWSYTYAYFSNWKSDNQKHLFEYHQGELEKNLDILQTKTEDINLTQFKNNTDNDT
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LTASLYPSHPLAMTYLQNKWIQTDTLKTHELYNNDFIRASVNANYNLQSGNIVMSDIM
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PEI EEK I I EVPQVQY I EKLVEVPHVILQEKLIHIPK PVIHERIKKCSKTIFOEK I VEV
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VSCFCNKNVQGNRQTNCY SLSGSCMCNPRTMGELKEKTNTMLHNPRI EQVFKPKIVKN
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                                                                                                                                                                                                                                                                                                                                                                                  /LKTSLHNDFEDDIITKECIDLKCNKIIKKNDWKNICEEKDYEKYLYTLLHIYIKKSK
                                                                                                                                                                                                                                                                                                                                                                                                           DLKKCPNKPCPY I IQSVMLNNNVICKCGYHFCFECLHEFHRPLLCSY IKKWY BLENN
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NNYENFENHQIKLYEQIIKEEQQNEKSNSKCCNYFCDK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(21152. .23273,23390. .23604,23713. .23862,
23997. .24194))
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/note="predicted using hexExon; MAL3P2.7 (PFC0190c), PAST
                           Hypothetical protein, len: 594 aa; Similarity with a number of hypothetical proteins from model organisms. C. elegans hypothetical protein (TR:001963) BLAST Socre: 361, sum P(1) = 4.0e-47, 35% idenitity in 227 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"predicted using hexExon, MAL3P2.5 (PFC0180C),
Hypothetical protein, len: 895 aa"
/codon_start-1
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   /note="predicted using hexExon; MAL3P2.4 (PFC0175w),
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lypothetical protein, len: 526 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRDIQQITQMIDIFFKNICEFMENNFV"
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                                                                                                                                                                      /protein_id="CAB38990.1"
/db_xref="G1:4493881"
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/gene="PFC0185w"
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DD 136567 GAAGTATATAAGTTTTCCCACTATATATATATTGTATATAATAATATTACCATAGTACC 136508
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                                                                                                                                                                 136924 TAAATATATATATATATATATATTATCCCCATTTTTGATGCTTTATTCATTATTCAATTT
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 Length 153098;
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                                    Indels
Score 91.2; DB 33;
Pred. No. 0.0013;
); Mismatches 508;
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4.2%;
nilarity 45.7%;
Conservative 0
                 Best Local Similarity
Matches 432; Conserv
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18-APR-1994

PLN

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Yeast (S.cerevisiae) mitochondrial Ser-tRNA and ATPase proteolipid
                                                                 transfer RNA; transfer RNA-Ser. mitochondrial DNA; cytoplasmic petite mutants
                                                                                                                                                                                                         sednence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tzagoloff, A., Nobrega, M., Akai, A. and Macino, G. Assembly of the mitochondrial membrane system. Organization of yeast mitochondrial DNA in the olil region Curr. Genet. 2, 149-157 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tatgatttcagggcgcaaaaatgcgagtacttaataaaattttacatttaaattagaatt 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tatgitcitcaaaitagaactigaaattattaattataaattaaaacigaaaacaattiggi 315
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                                                                                                                                                                              Assembly of the mitochondrial membrane system. The DNA is mitochondrial Arpase gene in Saccharomyces cerevisiae J. Blol. Chem. 254, 4617-4623 (1979)
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5' to SatII site, at Wild-type map units 79.1.
                                          ATPASE; proteolipid; transfer RNA; transfer RNA-;
Yeast (S.cerevislae) mitochondrial DNA; cytoplass
(rho-) ds400/a3 [1], ds401 [2],
Mitochondrion Saccharomyces cerevislae
Eukaryota; Fungi; Ascomycota; Saccharomycetales;
Saccharomycetaceae; Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Saccharomyces cerevisiae"
/organelle="mitochondrion"
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Pred. No. 0.003
0; Mismatches
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/db_xref="SGD:S0007274"
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/db_xref="GI:343939"
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.372. .1602
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                                                                                                                                                                     (bases 1026 to 2806
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llarity 45.7%;
Conservative (
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Direct Submission
Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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and Barrell,B.
                                                                                                                                    3987 ITATATTAATTTAATTTTAAAGTTATTTTTATAATAATTAATTAATTAATTAATTTATCAT 3928
                                                                                                                                                                                                                                                                                3927 TTATAGTATTTATAATTTCTATATTTTTATAATTATAATTTGTAGATTTCAATTAT 3868
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1 (bases 1 to 67970)
                                                                  316 atcaattcat--atacatgcttagtaataaaatgcgataattaattgataaatctgcaaa
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //octe="MALIP3.01, conserved hypothetical protein, len: 412 aa, similarity: UPF0006 family eg to YBL055C/YBL0512/YBL0511, YBF5_YEAST (418 aa), fasta scores: opt: 316, E(): 1.1e-12, (33.2% identity in 271 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOIKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKMFDGVYNSKKHENDLQNVLNRAK
NNNVDKIIITCTCLAEIDKSLKICETYDPEGKFLYLSAGVHPTNCYEFIDKNKHEEKE
IIAKKEYEEFIKYFKNEQVENSKMENGNKKICDGEKDMNLNEILLEKNLDIIPGFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MKLLNNRFVVLCPIIILFFLNSVVLGNNNRNNINFHETENAAK
AMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSQTDLFR
KKOEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ranslation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEKDKEYLENLKNKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVVVWFN
LPMFLHMRNCSETFFKIVDIYKFLFFKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
On Dec 16, 1999 this sequence version replaced g1:5763807. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSLKSLENINAVKKIPLNLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roduct="conserved hypothetical protein, UPF0006 family"
rotein_id="CAB63556.1"
b_xref="G1:6594244"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MAL1P3.03, putative ABC transporter, len: 1822 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region of very high [A+T] content"
                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(1748. .2598,2748. .2848,2990. .3276))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     donor sequence, atg/gttaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"potential splice donor sequence, aaa/gtaaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MALIP3.02, hypothetical protein, len: 163 contains possible signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"potential splice acceptor sequence"
complement(2984. .2989)
/gene-"MALIP3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="potential splice acceptor sequence" complement(2742...2747)
/gene="MALIP3.01"
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rotein_id="CAB63557:1"
                                                                                                                                                                                                                                                                          /organism-"Plasmodium falciparum"
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/protein_id="CAB63558.1"
/db_xref="GI:6594246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="potential splice
complement(2849. .2861)
/gene="MAL1p3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2599, .2610)
/gene="MAL1P3.01"
                                                                                                                                                                                                                                                                                                                                                                                              complement(1748. .3276)
/gene="MAL1P3.01"
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4884. .20352
gene="MAL1P3.03"
                                                                                                                                                                                                                                                                                                                /strain="3D7"
/db_xref="taxon:5833"
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1. .67970
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gene="MAL1P3.02"
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                                                                                                                                                                                                                                                                                                                                                                           chromosome="1
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        COMMENT
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Comptement()2170. (24.77), (24.6-8MALIP3.04). (24.6-8MALIP3.04). (25.6-8MALIP3.04). (25.6-8MALIP3.04). (26.6-8MALIP3.04). (26.6-8). (26 /protein_id="Cab63559.1"
/db_xref="G1:6594247"
/tanslation="MKKSTYFINVTILLFLTYYNYDTFSKTKFNNNIKIDIN
FKRAISAESEGKYPWEEDFCLILNEEELIRPEHNOSPYLPEHYENIDKINELSINS
TKIWKETIKKARONYEKETDNMNHNWRDFWMHYKWANIYLYKVHKLINITLKDLTNPI
HDKEETITTHIKWIQEDIEYFLFNLQVEWLRILTLEEFYKNKE" YISFLKDFKVFSGLVVVMIMFFHLFFBALLHFYFHLFTINLKVSLMYFLYKINLCSNN NHLONPDAFYNTYRKFSSQTEIDEISRDFLSIGKNASSSSSGIKNNNKNIDNNKFVEN /translation="mrikmnsgiffikllicispicvfecfnkcmisyrkbllmysen CFnysidrslaegssesketkvkbipniellkslninyeeyekmkeivgsfmbnnnln FKGSISLETYLWYFQQVGFVLLTSVVIFMLISIFTDEIKFVFLTMMSIISKNNKEHSD IILIYFFVFKRFSRGCKEAQRLYLSCHTPLCNIYSNALSGKNIINIYKKNTYHLDVYE DY I INFIKSTKKMEKDSLNENRSLPNVNI YNIMFSDVPSVTFFVTSCINLFNVFVK I F MSFYVFHIKIGSNSVGIAIWLSIALYSAMILFEFLPSLFKSKYLIYRDKRIDNMHVL YLKDRLNKKEEIKFTSIIMPLYVYKILISNVANFPNLVNNVMEGIVNIKRLNNYINDH KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINFN LKRNSLAIIIGNVGSGKSAFFHSILGDFNMTHGNLYIENFFKKMPILYVPQNSWLFMG NIRSMILFGNEYNPLIYKYTILQSELLNDLSTIEHGDMKYINDDHNLSKGQKVRICLA RALYEHYIHMHKLCTDYEKKLIQPNEILDKDLINNKNISSYNNKKSKLVNYNIPFNEN YLQKCLMDDNNFYLYLLDDIFTSLDPSISKKIFSNLFCKEDNISFKDNCSFIISMNKS TILQKQVRYLEYF, VILPIISL VTSGICFSMIIYGNITSAIK VHNNILY SILNAPLY IF LSSLLIYMIRDCIFIFPFV LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL NVITTOTYKEKNENISDKISAIVEYKNVSLSSIINSSQDDESKKKYGIKFENVYVSYK KITVEGRDIRTYNRKGEDSIIGILAQSSFVFYNWNIRTFIDPYNNFTDDEIVHALKLN KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI LYYNDIKNYFMYRTRYNEDYNIVVDKTFLONENITSHDDGTSHNLKHLKNVIKNKLTN MFKYFFFYHKMNYHKNIINKOILSGLLKNVDDNTNKKICFQEHKSNSTYNYNSSHIHE **TLDNFLIEDILDNVQYEVNIFEIQDKTLKYRGNISEYMEKNNLNITKESHWGYSNLNI** IDYTRIKLFDEVELNHVKHSNKMIYKEAYFVKGNTESVSFEIDSINKEYIKKMKKKNY HYINNFRISYFFKWLINIWASLYIKIFILLTTYIIMHPHLYASGIIKLYKEKNYVRI RHKYKIILIDEI PI FNLNNSVHDELNSFLIGKAKSFNYI I RNHFPNNTVLI I SHHANT KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINI /note="region containing small subunit, 5.8S and large subunit rRNA genes and spacer regions" 23896, .31533/gene="rRNA" KKEHMNKNNKDNNNNNNSNKDDHININMNDNHRNYNDINLGPNSTDDSPTVSSI GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRYLSLVR aa, /note="potential splice donor sequence, aaa/gtatat" /product="conserved hypothetical membrane protein, MAL1P3.04" jóin(36657. ,36743,36864. ,37343) /gene="MAL1P3.05" /note="MAL1P3.05, hypothetical protein, len: 188 /note="potential splice acceptor sequence" complement(32669, .32674) /gene="MALIP3.04" /product="hypothetical protein, MALLP3.05" /protein_id="CAB63560.1" /db_xref="G1:6594248" SCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD" YNNNLGNIINRFIIDISAFDYGFLKRIYKAFFIFFRCI complement(32477. .32486) /gene="MAL1P3.04" complement(31966. .32775) YTLDTYTSNNSDKEEIVKPLYKD1 /gene="MAL1P3.05" /codon_start=1 /codon_start=1 23896. .31533 /gene="rRNA"

9477

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Tamaki, T., Kurdi, O.B., Conway, A.B.
aaacataacatggatatctccttaccaatcatactaattatttgggttaaatattaatc 932
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Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                           ATTAATTAATTAAATAATTAATTTATTATTATTTAATTAATTTAATTTAATTT
                                                      taatcggtaacattagactttcaaaatcatttttaacccctaaacagtaaatttgaagga
                                                                                                                                                                    TGTAATTTATTATAAAATATAATTAATAA--AAATATAAATAAAATGAAAATAT
                                                                                                                                                                                                                                                                                                                                                          ctacacattgaccattgaaaagttcgttctcccatgggtaaccagatcaaactcacatcc
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                                                                                                                                 Hyman, R.W., Oin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pleces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9118 ATATAATATAAATTGTTTTATTTAAATTATTATATAATATATATTTT 9069
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Unpublished
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Hyman, R.W., Fung, E.L., Qin, F.,
and Davis, R.W.
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Plasmodium falciparum
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KEYWORDS
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QGGCGIISSVHETSNDTKDNDKENISEDKKEDHQQEEMLKTLDKKERKQKEKEMKEQE
IANEVLKNIHSFTNIENIFSLINDSSKSPVLKTFLKEFGSIFPHMLNNVPKLLFDLCQ
                                                                                                                                                                                                                                                                                                                                                      /translation="MNVLFLSYNICILFFVVCTLNFSTKCFSNGLLKNQNILNKSFDS
                                                                                                                                                                                                                                                                                                                                                                         ITGRILLNETELEKNKODNSKSETLLKEEKDEKDOVPTTSNDNLKNAHNNNEISSSTDP
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HDK ENBETMQQPDQTS EETNNE I MV PLPS PLTDVTT PEEHK EGEHK EEEHK EGEHK EGEHK EGEHK EGEHK EGEHK EG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>EQLIGTIGRVNVVPRRDNHKKKMAKIEEAELQKQKHVDKEEDKKEESKEVEEESKEVQ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote—"MALIP3.06, garp, len: 673 aa, similarity: almost identical to GARP_PLAFF (678 aa), fasta scores: 97.6% identity in 678 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9885
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/note="potential splice donor sequence, aag/gtaaca"
                                                    /gene="MAL1P3.05"
/note="potential splice donor sequence, aag/gtatga'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 ttaatttattattattagaaatattaattagaaaattttgaatccccgatttctcct
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                                                                                                                                                                                   .40284))
                                                                                                                         /note="potential splice acceptor sequence" complement(38049, .40284)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="potential splice acceptor sequence" complement(40204, .40209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                      /gene="garp"
complement(join(38049, .39995,40210,
                                                                                                                                                                                                                                                                                       /product-"hypothetical garp protein"
/protein_id="CAB63561.1"
/db_xref="G1:6594249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89.6; DB 33;
Pred. No. 0.0027;
0; Mismatches 544;
               RNPLHIILGLIVILAAIYVFENFKNFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(39996. .40005)
                                                                                                         /gene="MAL1P3.05"
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/gene-"MAL1P3.07"
                                                                                                                                                                                                                                                                               /codon_start=1
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ilarity 47.3%;
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9119

+** SEQUENCING IN PROGRESS

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Matches 534; Conservative
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TITLE
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soon as it is available and the accession number will
                                                                                                                                                                                                          Length 104992;
                       58642: contig of 58642 bp in length
58842: gap of unknown length
91011: contig of 33169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length.
                                                                                                                                                       405 others
                                                                                                                                                                                                       Score 89.6; DB 41; Length
Pred. No. 0.0023;
0; Mismatches 574; Indels
                                                                                                                 /organism="Plasmodium'falciparum"/db_xref="taxon:5833"
/chromosome="15833"
9326 c 9564 g 41411 t 40
                                                                                         Jocation/Qualifiers
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Best Local Similarity 47.3%;
Matches 534; Conservative
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Conway,A.B. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC004157 130281 bp DNA HTG 15-MAR-2000 Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                           tattttttttaatttcttaaaaaatgttgcaagacacttattagacatagtcttgttctg
                                                                               actcacatc----caaacataacatggatatctccttaccaatcatactaatttt
                                                                                                                                                                                       gggttaaatattaatcattatttttaagatattaattaaga-aattaaaagattttttaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Mar 15, 2000 this sequence version replaced gi:6652498
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 130281)
yman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
irect Submission
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3 67462: gap of unknown length
3 82485: contig of 15023 bp in length
6 82685: gap of unknown length
5 130281: contig of 47596 bp in length.
Location/Qualifiers
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47.3%; Pred. No. 0.0022;
iive 0; Mismatches 574;
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100027 TTAATTGTTTAATATTTATTATTATTTTAATATATATTAATTAATTAATTAATTATTA 100086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90666
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29 ataaaatgatggctaaaattggtgtgtgattggaacgatatctgtttattatgatttcaggg
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Drosophila melanogaster chromosome 3 clone BACR03115 (D765) RPCI-98 03.I.15 map 96B-96B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 133 unordered pleces.
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For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a "working draft' sequence It currently consists of 133 contigs. The true order of the pieces.

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker.S.E., Agbayani, A., Arcaina, T.T., Baxter.E., Blazej, R.G., Butenoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim. E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Paclifer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Stirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and
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                                                                                                                                                                                                                                                                                                                                              Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                                                                                                                                                                                                   terygota; Neoptera; Endopterygota; Diptera; Brachycera;
                           Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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Query Match
4.1%; Score 89; DB 55; Length 161891;
Best Local Similarity 41.2%; Pred. No. 0.0024;
Matches 432; Conservative 0; Mismatches 615; Indels 2; Gaps

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Plasmodium falciparum MAL3P7, complete sequence. AL034559 AL008974 AL008975 AL008981 AL008983 AL009015 AL010138 AL010143 AL010146 AL010154 AL010157 AL010160 AL010165 AL010169 AL010187 AL010189 AL010207 AL010208 AL010214 AL021885 AL021888

11-FEB-2000

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253307 bp

PFMAL3P7

RESULT 14

PFMAL3P7

DEFINITION

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Lawson, D., Bowman, S. and Barrell, B.

Direct Submission
Submitted (17-DEC-1998) P. falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 ISA, UK
On Apr 29, 1999 this sequence version replaced gi:4493963
For more information about this sequence or the Malaria Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 253307)
Oliver, K., Bowman, S., Harris, D., Lawson, D., Quail, M. and Barrell, B.
Unpublished
                                                                                                                                                                                Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M. Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyk, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J. Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A., Squares, S., Salston, J.E., Whitehead, S., Woodward, J., Squares, R., Squares, S., Barrell, B.G.
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5457. . 6743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinesin-related protein, len: 1201 aa; Similarity to
kriesin-related protein. D. melanogaster kinesin-like
protein 72A (TR:991945) BLAST Score: 664, sum P(2) =
1.96-67; 28% identity in 707 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-"predicted using hexExon; MAL3P7.1 (PFC0860w),
                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    see http://www.sanger.ac.uk/Projects/P_falciparum
Location/Qualifiers

    1. 253307
    Organism-"Plasmodium falciparum

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                                                       malaria parasite P. falciparum.
Plasmodium falciparum
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clone="MAL3P7"
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GI:4725992
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AL034559.3
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CDS

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/translation-*MGLFDKIRNIEKLNEAELKNIGNNDSSWHDQYRDSSYIYIGNLD
NRLTEGDIVIVFSQYGEPIDVNLVRDNETGKSKGYCFLSYADQRSTILAVDNENGYKL
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DDEDDDDDDSVDIKYKRHKEKRKSLLTKKYDKKEKHKRKSDHRDKHRREN
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// LIDIREYGENTDLDEVLKLYNTIMEGLTWGKAHKKTPFREGLFKLQVKKQMDDDEENYD
TSIYIYIYYWLFVSCVIVDDLVNTDELIETIENIGLDNEOLQKKKQMDDDEENYD
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YFFNDININLKQNFINFNTVDDLSFNIYFNEWYYFSFFIVLEYQFNSFILNYNADILK
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                                                                                                                 /note="predicted using hexExon; MAL3P7.2 (PFC0865w),
RNN-binding protein, len: 310 aa; Similarity to C.elegans
RNN-binding protein. C.elegans RNN-binding protein
(TR:Q18318) BLAST Score: 378, sum P(1) = 3.8e-35; 37%
identity in 297 aa overlap."
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Elongation factor 1-beta, len: 181 as: Similarity to
elongation factor 1-beta. A.salina elongation factor
1-beta (SW:EFIB_ARTSA) BLAST Score: 159, sum P(2) =
4.9e-16; 48% identity in 62 as overlap."
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aa"
                     Join(5457. .5577,5689. .5787,5923. .6077,6189. .
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'note="predicted using hexExon; MAL3P7.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
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/note="predicted using hexExon;
/lypothetical protein, len: 3004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="SPTREMBL:097278"
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/gene="MAL3P7.3"
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gene

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CDS

NQNEHISEKIQKANERDYKIELIPTASIYEHFKIILTFKNIELTNVELKYIINLLALI VNLKCDIHINCNQLSGGAKKKVELAINLLRDDKIIFLYKLNDNIDFCSQIYINIILKN ILLYNCEEDEHKDEYKDVYKDKYKDEYKDEYKDEYKDEYKDEYKDEYKDTYKDYEGYKYED PYWNNNQKYYKYVNNFIYISPQKKRIMKNNKNLNNYNIIYDILLKYNMHSFTQDDTLC SSLQINKLTNIHFLNLLYFKYQNINTKYLFIHNKLYKYQDLLKSPLCFNDKENISSIF LSFFLFLNICLNENTYKRILNYIYLIKLKKKKIQYIKHKTNKKLLNMLSNIKDLTIN /LYYFIYILCLFIVLYIFDYKEFLFMSFFCFLLLYGFNIFLSICLFSSLYLHSYILFL SFFNTSGDFVFLLINCIIYLSIVFYKLLQIIPSKERTDKKNESEKTNYEEIILNNSYN VGVQRKK EQKKNRYT FFLKNFY LSNK EYKQPK ENY EKNRNP FFYFI OKLFNLK RGNNV DENNTTMGIYKY GEKVDSNNY I SEDEININ QLNSEGYLKNDIYMNELNDNYNNDFDD KMRPYKIYTFSSIFNNDLNILYFFKYFFCNNKDNLKGSLQTIAYGQNYEINNKFINKK DILYYDYLYLENKNKITYKNYTTNIKNNEKKFYSFQIKLKGIRDSKIIDYVHMFFSIN KHAFARFEKVIKKMDDKNSKKPKKKKKLISPKDMPSNSIILFLENNVKRNVLNVHNL SIIKNYTYCIHKLENKQKIKDSTILTKYPIDFFNKLLLKLYNIENNIYEIIKHEQLYD ITINNKSHNKVSLYLSSLFNILTLOINENHKQTLQLYKKLLDCEININILSREVQNIN I LDG STYDNIK VVEDVKGNCDMNTLLYDKENKYNYLIKDIDNKNI REECNANFRLSKN VSYNNNEEEED I NGNI NYNDSNNI YITPKKNNKEEENNFLVKKLKKRIDTLNEPFNIK FFNFIFCGIISIVIYVLVILSYAYNNEILINLSHVLVCIFRIFDSFALSHVLNIRSLC LNVKRHMKHIDEDIMYEDMSNSNNFVIFGCFKKVYNQLSGDNNLNISDGIQSVCEDSN RVY EQDIQLYKGEGIYTNDENQFDDY IDKY SLYDLRGKEDRKQLRENMLKGRHGKNNY KFDESNDISYTSNDVLKGDDDMLSLRRNTKESKRNKNK INKKKKKENEL I LETYDI EK !YIFKTMKKKKYNSKKKKGNLISLCKFHKILLNLMIDKYSYLHSYLSRNKYISIFHLF Y EEKEDKNLINY NKY OKEFVCKDRKKNNTFITYDHIY SFMSFKKFSGKNISIDY NGSY KYHNFDINEVDNDIEEKIIKNTY RKKNLFNEHNY NKNIFY DNTKGQIILRIONIKRII FHEHEMRDFYINIYVFLSIVIFFCVFFERFKNEIENRKIFENFHVHOYIHYFOILLLE NTVDIEMQISEKSNIKEKMLYKETEIDKYYKGQSDDDNDEEKNFNKISQKYILKNLNI T NANOLGSNLSNSNY LECNISSNANSVNEP I I HSF I KEN I LK I KFG I ENFV I YTH I YT KFAICEVAYONIOKFIIKYKGIKKVYSEITSMNNYVFILKIYDNKHIFKILGKOKKKI /translation="MNIEERKKDIQTGIYEQEIFEELGQVLKEKFFKYINEANYEYYI 119198 281 /note-"predicted using hexexon; MAL3P7.5 (PFC0880c), Hypothetical protein, len: 478 aa" /codon_start-1 Gaps /note="predicted using hexExon; MAL3P7.6 (PFC0885c), 162 tagttttattagaaatattaattagaaattttgaatccccgatttctcctccttttctt cgctattcatcattttctaaccaaaccaatcttatatgttcttcaaattagaacttgaaa 282 ttattaattaaattaaactgaaaacaatttggtatcaattcatatacatgcttagtaat Score 88.8; DB 33; Length 253307; Pred. No. 0.0022;); Mismatches 522; Indels 9; QITEMLNKKLDANIQKWKNIKNETTPP" /db_xref="GI:4493967" /db_xref="SPTREMBL:097280" .22397) /gene="MAL3P7.5" complement(20964, .22397) complement(23721. .24665) /gene="MAL3P7.6" complement(23721. .24665) 'protein_id="CAB39026.1" complement (20964. 'gene="MAL3P7.5" ö /gene="MAL3P7. 4.18; Conservative Similarity 451; Query Match Best Local Si Matches 451; 222 gene CDS CDS

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YST ISSNHLKQSTINYFILYKNEMNNETLGYNKYNLNDDNIKKNLNNSYDKILKKLE

release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,

NOTE: This is a 'working draft' sequence.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

segments is not known; 800 n's separate segments

phage etc. Order of s

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Db 119617 TATATATATA-TGGAAAGATACTTCATAATATGTAATATATATATAAATATAAATAG 119675
                                                                                                                                                                                                                                                                                                                                                                      Db 119736 ATAGAGGGTTTCTTCTTA-AGCAAATTTGTATAAAATATAGGGGGGATATAAAATATAA 119794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 119975 AATATATATATATATATTTATTGAATAATCCTTTGTCATGTTTATTTTTTAATAAA 120034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 119795 ATATAAATAATATATATTTTTTTTTTAGGGTGGTATTCAAAGCAAAGCTTAAACAAAA 119854
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                                                                                                                                   tatttttcaaatttgatagactattttttttttgtaatttgacgaaccaaaaccagattt
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                                                                 ctctcctacggaccattctttgcacttcaactaaacgatggtcagaattggtggggattt
                                                                                                                                                                                                     acattagactttcaaaatcatttttaacccctaaacagtaaatttgaaggacaaaaataa
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Length 80518

Score 88.2; DB 31; Pred. No. 0.0038; 0; Mismatches 563;

4.18;

Conservative

464;

Matches 109

Similarity

Query Match Local

8800 others

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7591 g 27672

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BASE COUNT

/db_xref="taxon:5833" /chromosome="13" 6650 c 7591 g 2

/organism-"Plasmodium

/strain="3D7"

Location/Qualifiers

.80518

source

FEATURES

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19-AUG-1999

Plasmodium falciparum chromosome 13 strain 3D7,

DNA

80518 bp

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 15

PEMAL13PA

ROGRESS ***, in unordered pieces.

AL109815.2 GI:5763806

HTG; HTGS_PHASE1.

ORGANISM

REFERENCE AUTHORS Submitted (11-AUG-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge

Direct Submission

TITLE JOURNAL

CB10 1SA,

COMMENT

Barrell, B.

Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M.

malaria parasite P. falciparum. Plasmodium falciparum Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 80518)

On Aug 24, 1999 this sequence version replaced gi:5731892.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the

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Maximum Match 100%
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117:
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CNSODEVL 1101 bp DNA GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit

1101 bp

RESULT 1 CNSOOEVL/C LOCUS DEFINITION

6.0%; Score 95; DB 122; llarity 34.7%; Pred. No. 8.3e-07; Conservative 100; Mismatches 270; 299 t fly), genomic survey sequence. AL069706 /db_xref="taxon:7227 /clone_llb="RPCI-98" Location/Qualifiers 6 09 /clone="BACR29B23" Pl and EST libraries. (bases 1 to 1101) /note="end 91 c Submission al Similarity 197; Conserva AL069706.1 Genoscope 419 Query Match Best Local S Matches 197 VERSION KEYWORDS SOURCE ORGANISM source BASE COUNT ORIGIN AUTHORS TITLE 693 ACCESSION JOURNAL REFERENCE FEATURES COMMENT a ò g g a ò a ò ò g ALIGNMENTS SUMMARIES gb_gss13

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. the library in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP 573 taatcggtaacattagactttcaaaatcattttaacccctaaacagtaaatttgaagga 632 813 ctacacattgaccattgaaaagttcgttctcccatgggtaaccagatcaaactcacatcc 872 819 WATWTATWTATTTATWTWTWTTWTATTWTATWTATWWWTWWATWWWTAWAAWTATAT 760 873 aaacataacatggatatctccttaccaatcatactaattattttgggttaaatattaatc 932 879 TITITWITATWATATWATATTAWATTTTTWITWIATTWWIATAWWATWWIATWITT 820 699 ITITITITITIMAATITIMAATITIAATITAMWWAAIWAWITATITIAATAAWIAATITAAAT 640 The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information 753 tctaaaaacaaaatttcatggcagcatgcctcagcccatgaaaaaaaccttataaaaatat Drosophija melanogaster Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. melanogaster genome using these BACs. For further inform please see http://www.fruitfly.org The BDGP Drosophila Length 1101; Cancer Genetics at the Roswell Park Cancer Institute A more detailed description of 232 others Indels organism="Drosophila melanogaster" ò

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- Web: www.genoscope.cns.fr.
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- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information. please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                 CNSOOEVL 1101 bp DNA GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
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/db_xref="taxon:7227"
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1larity 35.1%; Pred. No. 2.6e-06;
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**Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/db_xref="taxon:7227"
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
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Pred. No. 7.5e-06
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please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EOSI dipsestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; no w sp. the same strain used for the BDGP's PI and ESI libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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from Drosophila melanogaster (fru
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de
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Live 92; Mismatches 154; Indels
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/db_xref="taxon:7227"
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BACN12P22 of DrosBAC library frof [IJy, genomic survey sequence.
AL104456 GI:5616067
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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llarity 32.0%; Pred. No. 1.8e-05;
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/clone_lib="DrosBAC"
/clone="BACN12P22"
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or fillters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
      FRANCE (E-mail : segref@genoscope.cns.fr
                                                                part of
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Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project
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40.5%; Pred. No. 3.4e-05;
iive 56; Mismatches 265;
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/clone_lib="RPCI-98"
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Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fullfly.org The BDGP Drosophila melanogaster BAC Ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoxI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain v2: on bw spp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                             Urosophila melanogaster genome survey sequence TET3 end of BAC # BAC # BAC # SAR08K10 of RPCI-98 library from Drosophila melanogaster (fruit AL063921
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
(bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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18.5%; Pred. No. 5.4e-05;
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- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR26H19 of RPCI-98 library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Location/Qualifiers
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Length 843;

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Length 1101;

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Similarity
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
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collaboration with the Berkeley Drosophila Genome Project (BDG
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre C'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
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                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                    caaactcacatccaaacataacatggatatctccttaccaatcatactaattatt----
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Score 83; DB 122;
Pred. No. 7.9e-05;
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/organism="Drosophila melanogaster"

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Best Local Similarity
Matches 152; Conserv
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Ordect Grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSO161D 1225 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
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Muscomorpha; Behydroidea; Drosophilidae; prosophila.
1 (bases 1 to 1225)
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                                                                                                                                                     Length 1101;
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                                                                                    436 others
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; Pred. No. 8.6e-05;
90; Mismatches 133; 1
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/plasmid-"pBeloBAC11"
/db_xref-"taxon:7227"
/clone_lib-"DrosBAC"
/clone="BACN16D22"
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AL106171
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/clone="BACN15C18"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster BAC library was prepared by Kazutoyo Osoegawa and, Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGP The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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Pterygota; Neoptara; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 928)
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                                                                                                                                                            Length 1225;
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iive 93; Mismatches 180;
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Submitted (23-011-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@enoscope.cns.fr
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Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN15C13 of DrosBAC library from Drosophila melanogaster (fruit
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryopota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)
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                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                                                                                                                                                            84 g
                                                                                                                                                        /clone-"BACR27A24"
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                                                                                                                                                                                                                                                            Query Match 5.2%;
Best Local Similarity 31.1%;
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                                                                                                                                                                                        BASE COUNT
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project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tacaaaagcattcatcatttaatacattaaaaaatatttaatactaacagtagaatcttc 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 860 caaactcacatccaaacataacatgatatctccttaccaatcatactaattattttggg 919
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
1 (bases 1 to 1043)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1201;
                                                                                                                                                                                                                                                                                                                                                           120 others
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                                                                                                                                                                               melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 81.2; DB 123;
Pred. No. 0.00016;
5; Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                        336
                                                                                                                                                                     /organism="Drosophila m
/plasmid="pBeloBAC11"
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/clone_lib="brosBAC"
/clone="BACNISC13"
                                                                                                                    Location/Qualifiers
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Job time: 4339 sec
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project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBeloBACII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage 3P 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
Collaboration with the European Drosophila Genome Project (EDGP) -
thtp://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                            agacacttattagacatagtcttgttctgtttacaaaagcattcatcatttaatacatta 1126
                                                                                                                                                                                                                                                                                                                                                                                        887 tatctccttaccaatcatactaattattttgggttaaatattaatcattattttaagat 946
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                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTWTWTATATTATWWTWTWTWAAATATTTTTTATWTATATTTATWTATWTTTWA 727
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terygota; Neoptera; Endopterygota; Diptera; Brachycera;
uscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                  167 others
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                   melanogaster
                                                                                                                                                                                Score 81; DB 123;
Pred. No. 0.00017;
3; Mismatches 158;
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                                                                                                                    382
1. 1043
/organism="Drosophila m
/plasmid="pseloBAC11"
/db_xref="taxon:7227"
/clone="lb="lb="brosBAC"
/clone="hACN1JG11"
/note="end-right"
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ACN15E04 of DrosBAC library fr
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                                                                                                                    121 g
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                                                                                                                                                                                                    Similarity 41.2
3; Conservative
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CNS016CO/c
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                                                                                                                  BASE COUNT
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1067
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SOURCE

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1079 TITWITITITWIWATWIWITITITWIIWWAWIWIWWAWIWIATITITITAIATIWAAI 1020
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                                                                                                                                                                                                                                                                                                                                                       Length 1200;
                                                                                                                                                                     187 others
                           melanogaster
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                                                                                                                                                                                                                                                                                                          61; Mismatches 147;
                                                                                                                                                                                                                                                             DB 123;
0.00025;
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1. .1200
/organism="Drosophila
                                               plasmid-"pBeloBAC11"
                                                                      db_xref-"taxon:7227
                                                                                       /clone_lib="DrosBAC/clone="BACN15E04"
/note="end : T7"
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Matches 132; Conservative
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APPLICANT: DZIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SOREN;
YUUST, JENS; RIENBEK, KLAUS, WIND, ANNETTE; JAKOBSEN, PALLE H.
TITLE OF INVENTION: MALARIA ANTIGEN
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
FILING DATE: 18-SEP-1989
US-08-107-755A-1
US-07-991-867B-1
US-08-544-332-1
US-08-449-315-36
US-08-449-315-36
US-08-449-315-36
US-08-449-315-36
US-08-455-265A-36
US-08-455-244-36
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US-08-336-345-2
US-08-647-655-2
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Matches 167; Conservative
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8457
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LENGTH: 3095
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Best Local 5
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(without alignments)
1933.669 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Sequence 36, Sequence 37, Sequence 37, Sequence 17, Sequence 17, Sequence 17, Sequence 17, All Sequence 126, All Sequence 17, All
                                                                                                                                                                                                                                                                                     atcgatagagacatgttatt.....gtttttgaagtataaagatg 1574
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/ina/5A_COMB.seg:*
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US-08-487-826B-13
US-08-883-795A-36
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8-764-100-20
8-565-907A-1
8-910-551B-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 1000000
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19124
11186
6243
3138
6655
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19124
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8920
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4970
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Post-processing:

Database :

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Minimum DB : Maximum DB :

Scoring table:

Searched:

Perfect score:

Sequence:

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Run on:

340

Sequence 13, Application US/08487826B Patent No. 5993827 GENERAL INFORMATION:

Sequence 126,

US-08-413-118-126 US-08-473-446-126

49 48.4 48.4

07-593-657-14 .08-107-755A-1

53.8 53.8 52.6 52.6

Score

Result Š 2511.2 5511.2 5511.2 5500.2 5500.2 5500.2 56000.2 5600.2 5600.2 5600.2 5600.2 5600.2 5600.2 5600.2 5600.2 5

RESULT 2 US-08-487-826B-13

Gaps

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964 aagattttttaaaaaaatgtataaaaattatattattcatgattttcatacattgattt 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 ITATTAGAAGTATTTTCATTTTAATTTTTTTTAAAAGTTATATATCTTTAAAAAGATAT 420
                                                                                         Biocontrol of Fungal Soilborne Pathogens
by Pythium oligandrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
0.018;
73;
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54.2; DB Pred. No. 0.018 0; Mismatches
                                                                                                                                                            STREET: 2421 N.W. 41st Street, Suite A-1 CTTY: Gainesville
                    Application US/08731722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09056075
Patent No. 5955368
                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.4%;
Best Local Similarity 59.3%;
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1186 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Whitlock, Ted W. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                 NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; INDIVIDUAL ISOLATE:
US-08-731-722-5
                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
-08-731-722-5/c
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APPLICANT:
APPLICANT:
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                                                                                             BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1264 ATTATAATATGTAAATTATTAATAAAATATTGTATAACATACAAGACTAAAAGAAAAC 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tttttaaaaaaatgtataaaattattattcatgatttttcatacatttgattttgata 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1149 agaatettettgtgagtggtgtgggagtaggcaacetggcattgaaacgagagaaagaga 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1444 TTAGTATTTTAATAATAAATCTTTTAAAAACTTCAAAACATTTTTGCATAAAATA 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1564 ATTAGAACAAAAGAATATTACAAAAAATAATAAAATTAAATTA 1607
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                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25.
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826R
                                                                                                                                                                        : Knobbe Martens Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                             ливек: US/08/487,826B
10-SEP-1993
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29,622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
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Best Local Similarity 47.7%;
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTORNEY/AGENT INFORMATION:
NAME: ISTACLSON, Ned
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             Newport Beach
California
                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (619)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: HYPOTHETICAL: N
                                                                                                                                                                                                                                                                     92660
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US-08-487-826B-13
                                                                                                                                                                        ADDRESSEE
                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                      STREET:
                                                        NPPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 3770 4013
CTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from cyHER INFORMATION: plasmid RP4"
US-09-056-075-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4%; Score 53.8; DB 4; Length 6243; 50.8%; Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
Expression System for Clostridium Species
                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 147;
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/056,075
                                                               SSEE: Quarles & Brady
?: 1 South Pinckney Street
Madison
                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGEWT INFORMATION:
NAME: Seay, NICHOLAS J.
REGISTRATION NUMBER: 27386
REFRENCE/POCKET NUMBER: 960:
TELECOMMUNICATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4OLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6243 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.8
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: double
                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                CORRESPONDENCE ADDRESS:
                                 SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                             53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                ADDRESSEE:
STREET: 1
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                                                                                                                                 COUNTRY:
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US-07-867-106-4 Sequence 4, Application US/07867106

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2713 AACTITAGTAATAAGAFCGATCTATACTTCAGTACGAACATAAATATGTATAAACCAAAA 2772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       783 cagoccatgaaaaaaaaccttataaaaatatotacacattgaccattgaaaagttcgttct 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 843 cccatgggtaaccagatcaaactcacatccaaacataacatggatatctccttaccaatc 902
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3138;
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                         NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.7%;
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 base pairs
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                               ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIOR APPLICATION DATA:
                                                                                                                                                                                    Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circular
                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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US-07-867-106-4
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Sequence 1, Application US/08446855A
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                                                                                                                                                                                                                                                         STATE: Vi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                      IS-08-446-855A-1/C
                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 TITATAATTAAAATTATAATTAAATATTITATAATTAAAATATTAAATAT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 TATAATTAAAATATTTATAATTAA--ATATTTTATAATTAAAATATTTATATAAATAT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
WUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; DB 4; Length 665; 0.033; ches 99; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin PC-
                                                                                                                            sequence 36, Application US/08883795A
Patent No. 5985607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                 STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ravelle, Micheline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (416) 364-7311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Rh 32
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Best Local Similarity 55.1
Matches 124; Conservative
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                       Canada
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Delcuv
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                                                                                              RESULT 6
US-08-883-795A-36
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1083 ta 1084
                                    2953 TA 2954
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1083 tagtottgttctgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatact 1142
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APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoy1
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          :: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 135;
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Pred. No. (
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                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537 AATTATAGGAACCACAATATTGGGGAGT 510
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; Sequence 13, Application US/08487826B
; Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.2
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3%;
Best Local Similarity 49.6%;
Matches 133; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: genomic
                                                                                                                                                                                                                                                                                     ZIP: 22201-4714
COMPUTER READABLE FORM:
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1062 ttgcaagacacttattagacatagtcttgttctgtttacaaaagcattcatcattaata 1121
                                  Genevieve
                                                                                                                                   E: BERESKIN & PARR
40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELECOMMUNICATION INFORMATION TELEPHONE: (416) 364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (416) 364-7311
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                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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R SEQ ID NO:
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Best Local Similarity 46.0
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                  APPLICANT: Delcuve,
APPLICANT: Awang, G
                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                    COUNTRY: Canada
ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                   GENERAL INFORMATION:
                                                                                                                                                                                      Ontario
                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2'
CLASSIFICATION:
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                                                                                                                                                                     Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CLONE: Rh
US-08-883-795A-36
                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                  STREET:
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                                                                                 Su, Xin-zhaun
Wellems, Thomas E.
VERTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
VERTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057 aaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattcatcatt 1116
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                                                                                                                                                                                                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                        E: Knobbe Martens Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51.4; DB Pred. No. 0.085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFRAX: (619) 235-0176
INPORMATION FOR SEQ ID NO: 13:
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10-SEP-1993
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US-08-883-795A-36/c
; Sequence 36, Application US/08883795A
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29,622
                                    Chitnis, Chetan
Miller, Louis H.
Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.3%;
Best Local Similarity 53.0%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19124 base pairs
nucleic acid
:DNESS: single
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                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                   m, Kim L.
                                                                                                                                                                                                                        CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                 APPLICANT: Wellems,
TITLE OF INVENTION:
TITLE OF INVENTION:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                            92660
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US-08-487-826B-13
                                                                                                                                                                                        ADDRESSEE:
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1002 tgattiticatacattigattitgataataataaatattittititaatitctiaaaaaatg 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 GTAATTATAAACATTTTAATTATAAAATATGTAATTATAAACATTTTAATTATAAATAT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 GTAATTATAAACATTTTAATTATAAAATATTTTAATTATAAACATTTTAAT-TATAAAATA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 TACTITAATTATAAAATATGTAATTATAAATACTTTATAAAATATGTAATTATAAAATAT 439
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Recombinant DNA Molecules and Expression
Vectors for Tissue Plasminogen Activator
39
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Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sat Sep

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965 agattttttaaaaaaatgtataaaattatattattcatgattttcatacatttgattt 1024
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505 ATTATTTATTTCTTATTAAAATATTATGAFTATTATTAAAGTAGAATAAGG--ATTACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 ATTITCIGITAAAAAATAAAACCITICICIATIGAAGAATTITTATAGCIACIGITIA 622
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by Pythium oligandrum
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51.2; DB 4;
Pred. No. 0.076;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                  :: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                               1122 cattaaaaaatatttaatactaacagtagaat 1153
                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UI
TELECOMMUNICATION INFORMATION
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.3
Best Local Similarity 54.3
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Whitlock, Ted W. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; INDIVIDUAL ISOLATE:
US-08-731-722-3
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2421 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32606-6669
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3429 ATTATTTATTTCTTATAAATATTATGATTATTATTAAAGTAGAATAAGG--ATTACA 3372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1025 gataataaatatattttttttaatttcttaaaaaaatgttgcaagacacttattagacata 1084
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                                                                                             Biocontrol of Fungal Soilborne Pathogens
by Pythium oligandrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3933;
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                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51.2; DB 4;
Pred. No. 0.076;
0; Mismatches 103;
                                                                                                                                                                                STREET: 2421 N.W. 41st Street, Suite A-1
CTTY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/731,722
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Sequence 3, Application US/08731722
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O'Sullivan, William
                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE: 1986-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%;
Best Local Similarity 54.3%;
Matches 125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Whitlock, Ted W. REGISTRATION NUMBER:
                                                                                                                                               NUMBER OF SEQUENCES: ECORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
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1042 tittaaitticttaaaaaaigitigcaagacacttaitagacatagictigiticigittaca 1101
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                                      Improvements in or Relating to Organic Compounds
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                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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Pred. No. 0.09;
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De Haan, Petrus T.
Gielen L., Johannes J.
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/032,235
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5773700116, Allen E.
REGISTRATION NUMBER: 34,490
                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08764100 Patent No. 5773700
                                                                                                                 E: Sandoz Agro, Inc.
975 California Avenue
                    Goldbach, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1: ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 334-3592
TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
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52.1%;
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Best Local Similarity 52.13
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 base pairs
nucleic acid
    Dirk
                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Ag
STREET: 975 Californ
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT: van Grit
APPLICANT: De Haan
APPLICANT: Gielen
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                                                                                                                                                         CITY: . Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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    Nucleotide sequence encoding carbamoyl phosphate synthetase II
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Pred. No. 0.11;
0; Mismatches 164; Indels
                                                                          E: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
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US-08-764-100-16
Sequence 16, Application US/08764100
Patent No. 5773700
GENERAL INFORMATION:
APPLICANT: Van Grinsven J., Martinus Q.
APPLICANT: De Haan, Petrus T.
APPLICANT: Glelen L., Johannes J.
                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-U1-1995
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47.
FLEECOMMUNICATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.2%;
Best Local Similarity 47.6%;
Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8920 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
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                                                            CORRESPONDENCE ADDRESS
TITLE OF INVENTION: . TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                               CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Gaps

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Search completed: September
Job time: 8407 sec
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               PPLICANT: Goldbach, Robert W.
ITLE OF INVENTION: Improvements in or Relating to Organic
ITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 103; Indels
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URRENT APPLICATION DATA:
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Pred. No. 0
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De Haan, Petrus T.
Gielen L., Johannes J.
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
RIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
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US-08-764-100-20/C
: Sequence 20, Application US/08764100
: Patent No. 5773700
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-MAR-1992
NTORNEY/AGENT INFORMATION:
NAME: No. 5773700ris, Allen E.
REGIGSTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1
                                                                                                            3: Sandoz Agro, Inc
975 California Avenue
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.2%;
Best Local Similarity 52.1%;
Matches 112; Conservative
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 Dirk
                                                                    NUMBER OF SEQUENCES: 2
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                                                                                                                                               Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                   ZIP: 94304
                                                                                                            ADDRESSEE:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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3738 AAAACCAAAAAATTTTTTTTTTAAATAAATAAGGCTCCGGCCAGATTTGGTCTAAGACC 3679
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0.12;
 Improvements in or Relating to Organic Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50.2; DB 2; Pred. No. 0.12; 0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1102 aaagcattcatcatttaatacattaaaaaaatatt 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3558 CAATCATTCTGCCTTATTTAATTTAAAACACATTT 3524
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANO. 2773700ris, Allen E. RATION NUMBER: 34,490
                                                                                                                                                                                                                                                                                                                                                                       US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                            us 08/032,235
                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: GB 9206016.9
19-MAR-1992
                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         E: Sandoz Agro, Inc
975 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.2%;
Best Local Similarity 52.1%;
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: .
APPLICATION NUMBER: US 01
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 857-11.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz AG
                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                            Palo Alto
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                 USA
                                                                                                                                                                                                     MEDIUM TYPE:
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2, 2000, 02:00:43

	Ltd.
4.5	Compugen
version	- 2000
GenCore v	(c) 1993
	Copyright

OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	September 2, 2000, 02:02:54 ; Search time 161.21 Seconds (without alignments) 2442.791 Million cell updates/sec
Title: Perfect score:	US-09-464-528-15
sequence: Scoring table:	i ategatagagacaigitaitgittitegaagtataaagaig 13/4 IDENTITY_NUC Gabop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 623170

311585 seqs, 125096042 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	•	٠			SUMMARIES	
Result		Ouerv				
NO.	Score	Match	Length	DB	. QI	Description
1	63	4.0	3101	!	002047	Sequence encoding
7	60.2	3.8	9789	-	T41852.	cDNA encoding Plas
9	59.6	3.8	1864	-	Q78892	Aspergillus nidula
Ω	59	3.7	1864	ч	N71405	Seguence of ANS-1
2	58.8	3.7	53585	ч	X20251	burg
9	58	3.7	110000	٦	X20248_05	Continuation (6 of
C 7	58	3.7	116277	-	9	Borrelia burgdorfe
8	57.2	•	3095	۲.	Q03875	Sequence encoding
6	57	3.6	6124	-	Q03568	
c 10	56.4	3.6	5849	-	V33135	
c 11	٠.	3.6	2418	1	027886	P.falciparum GBP13
12	د	3.6	1864	-	N71405	Sequence of ANS-1
13	26	3.6	4590	-	N60472	Sequence encoding
. 14	S	3.6	19124		T72882	Plasmodium var-7 g
c 15	55.	3.5	2104	Н	025273	Sequence encoding
16	55.	3.5	1671	-	024134	\sim
c 17	54.	3.5	4590		N60472	Sequence encoding
c 18	54.	3.4	. 1186	-	V29580	О
~	Э.	3.4	909	~	T31530	
20	Э.	3.4	5760	-	N50530	
21	53.6	J. 4	2503		Q53480	pNPX30 xylanase cD
7	ω.	3.4	3775	-	V74549	Staphylococcus aur
	щ	3.4	6124	-	003568	
~	53.	3.4	1393	-	N60225	
~	S	3.4	53585		X20251	Borrelia burgdorfe
~	53.	3.4	110000	-	X20248_03	nuat
27	2	•	605	~	m	Human 3' apolipopr
c 28	S	3.3	1470	-	055185	MS-Le1610 Vector.
29	S	3.3	26811	-	n	Borrelia burgdorfe
30	52.	3.3	110000	-	œ	Continuation (4 of
31	2	3.3	. 1826	급	V37413	
32	52.	ж. Э.Э	1826	-	V29477	Orpinomyces cellul
c 33	52	3.3	8920	-	062924	Carbamoyl-phosphat

	Malaria-specific g	SERP gene. Recombi	Borrelia burgdorfe	Continuation (7 of	Shuttle vector pMU	cDNA encoding Plas	Plasmodium var-7 g	Borrelia burgdorfe	Plasmodium berghei	Pythium oligandrum	Pythium oligandrum	Continuation (5 of	
	N81157	022999	X20253	V21209_06	011712	T41852	T72882	X20361	V33136	V29578	V29578	T58840_4	
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	3975	3975	26811	110000	3138	9789	19124	783	1711	3933	3933	110000	
	3.3	3.3	3.3	3,3	3.3	3.3	3.3	3,3	3,3	. a	3.3	3.5	
	51.8	51.8	51.8	51.8	51.6	51.4	51.4	51.2	51.2	51.2	51.2	51	
	34	35	36	37	38	39	40	41	42	43	44	45	
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ALIGNMENTS

AAC encodes Aspartic acid

/transl_except= 3461. .3463

misc_feature

*tag=

misc_feature

transl_except- ATT encodes Leucine 909. .2911

/transl_except= GAA encodes Glutamine 5546. .5548

encodes Arginine

except - CCT

transl

misc_feature

misc_feature

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2622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTTTCCTATATAAAATTTAAAATGAAAAATATATATTAAACTAATTAAGAAAAAAT 2742
                                                                                                                                                            TATITGIIGATTACIIITAIGIITATTCICCTITAAITTATAATCATITATATATATATA 2454
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                            attataattaaactgaaaacaatttggtatcaattcatatacatgcttagtaataaatg
                                                    408 acaaattttgtcgttttcatggtgttggtctgaggaggatttggcactatagaactctcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2922 GIGGAATITITAAAAATCATCAATTATITITGACTCCCGTTTTTCATCATTTTGTTCAT
                                                                                  cgataattaattgataaatctgcaaaagattttacaaatatcttcagaaaaaattaata
                                                                                                                                                                                                                                                                                     TTCATATATTTATTTGTTAATTTAAACATTTTAGTAGAATAAAAGAAACCTATAATAAA
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/transl_wxcept= GGA encodes Tryptophan 7754. .8478 /*tag= n

27-APR-1995; US-430908. (APRY-) AFRYMAX TECHNOLOGIES NV. Baruch DI, HOWARD RJ, Pasloske BL; WPI: 96-497376/49.

P-PSDB; W00384

transl_except= ATT encodes Asparagine 278. .6280

except- TTC encodes Isoleucine

trans]

misc_feature

-except= ATA encodes Tyrosine

6263. .6265 /*tag= 1 /transl_exc

misc_feature

misc_feature

transl,

-except- AAC encodes Lysine

1_except- AAT encodes Lysine
.6259

*tag= transl

misc_feature

ATA encodes Histidine

transl_except=

misc_feature

misc_feature

intron

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protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patients suffering from malaria. Nucleic acids derived from the PfEMP1 gene can be used as probes and primers to identify a plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different practice which the PfEMP1 polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the PfEMP1 protein of the MC type of Plasmodium falciparum. An
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PfEMP1 protein of the MC type of Plasmodium falciparum. An alternative, truncated version of the coding sequence (a cDNA clone)
                                                                                     Disclosure; Figure 12; 149pp; English.
A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte
membrane protein 1 (PfEMP1) or active fragments or analogues of tl
New Plasmodium falciparum erythrocyte membrane proteins - used develop products for the diagnosis, treatment or prevention of malaria parasite infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 60.2; DB 1; Length 9789; Pred. No. 0.058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1837 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1393 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%;
ilarity 48.2%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is given in T41853
Sequence 9789 BP
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CDNA encoding Plasmodium falciparum erythrocyte membrane protein. Plasmodium falciparum; erythrocyte membrane protein; malaria; detection; identification; treatment; prevention; parasite; ss.

T41852 standard; DNA; 9789 T41852; 20-FEB-1997 (first entry) Plasmodium falciparum MC type. Key

326. 9497 / tag a //tag a //product Erythrocyte membrane protein 518. 520

misc_feature

misc_feature

/transl_except= GTA encodes Tyrosine 656. .658

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1281 TAAAACTGAATAATATTAAAGAATAGTATTTATCTAAGTATAACTTAAATCTTAGTAATA 1340
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                                                                       1088 ttgttctgtttacaaaagcattcatcattaatacattaaaaaaatatttaatactaacag 1147
                                                                                                         1148 tagaatettettgtgagtggtgtgggagtaggcaacetggcattgaaacgagagaaagag 1207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Include secretory signal sequences that are native or foreign to blactosurer, Fig 13A-13B; Sopp; English.

The sequence represents the A. nidulans ANS-1 sequence which is included in the construction of transformation vectors for recombinant protein expression and secretion from a filamentous fungus host. The sequence increases the transformation efficiency of the vector. This illustrates the main claims of the patent, which provide a vector containing (1) DNA encoding a heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vectors and DNA for expressing polypeptide(s) in filamentous fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttattagaaatattaaattagaaaattttgaatccccgatttctcctccttttcttcgcta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide (chymosin, prochymosin, preprochymosin, Aspergillus niger glucoamylase, Humicola grisea glucoamylase or M. miehei carboxyl protease) and (ii) a secretory signal peptide, and a filamentous fungus (Aspergillus, Trichoderma, Neurospora, Podospora, Endothia, Mucor, Cochlobolus or Pyriolaria, especially nidulans, A. awamori or T. reesei) transformed with the vector for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttcatcattttctaaccaaacca-----atcttatatgttcttcaaattagaact
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                                    3.8%; Score 59.6; DB 1; Length 1864; 51.9%; Pred. No. 0.073; ive 0; Mismatches 144; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                732 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawlis VB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 G;
                                                                                                                                                                                                                                                                                                                                                                                                                          Vector; transformation; protein secretion; ds. Aspergillus nidulans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray GL, Hayenga KJ,
                                                                                                                                                                                                                                                                                                                                                                                                           partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant protein (enzyme) production.
Sequence 1864 BP; 819 A; 193 C;
                                                                                                                                                                                                                                                                                                                                                     Q78892 standard; DNA; 1864 BP
                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus nidulans ANS-1
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1985; US-771374.
07-JUL-1986; US-882224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cullen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-1986; 201751
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1194 AGNTGCTAGCTTANGTAGTTAATATTAAAATTAAAATTAAAATTAAGTATATGTCTGTN 1135
                                          1341 CTAAAAATTTAATTAATTAAATAATATAAATATAAATTGACCTTGAAACTGTTACT 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1554 ATTICTAAININITAGGAAGNINIATCTATICTICTTAATAATCTTAATAATTITTATA 1495
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337 gtaataaaatgcgataattaattgataaatctgcaaaagattttacaaatatcttcaga 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the DNA sequence codes for bovine preprochymosin, M. methel preprocarboxyl protease or A. niger preproglucoamylase. Also new are vectors consisting of the DNA sequence plus an operably-linked signal sequence. The vectors may also include a sequence which increases transformation efficiency, e.g. ANS-1. Sequence 1864 BP; 786 A; 210 C; 44 G; 732 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 gaaaattttgaatccccgatttctcctccttttcttcgctattcatcattttctaaccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1494 GAGNTITATTANNNNTAGAGTATTTTTTATAGTTTCTTAAGTAATTTATTNTTAGNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1434 AGTTATTATAATTAATAATATATAATAAAGTTTAGTAANAGTTTNAAGGTCAANTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aatotgcaaaagattttacaaatatotttcagaaaaaattaataacaaatttgtcgttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1254 TAATTATTGTNTANNNTGGNTAGTATATCTTATTTATAGTATAATATATATNTAGGNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cullen D, Gray GL, Hayenga KJ, Lawlis VB;
WPI; 87-095049/14.
New DNA sequences for expressing polypeptide in filamentous fungi
- with secretion of prod. from the cells, and new vectors and
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                                                                                                                                                                                                                                                                                                                                                  transformation efficiency. Aspergillus expression vector;
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42.8%; Pred. No. 0.09;
tive 0; Mismatches 583; Indels
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Enzyme; fungal expression vector;
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Best Local Similarity 42.8
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US-882224.
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07-JUL-1986;
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Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Borrella burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly. Lyme disease Claim 1; Page 801-831; 1128pp; English. 820248 to X20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for
                                                                                                                                                                                                                                                                                                                                                                 ATAATATTTTTNTAGTAGTGTGTGTTAATATAAGAGCTTTAAAAATTATTCTTAATTAG
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                                                                                                                                                                 ctattttttttttgtaatttgacgaaccaaaaccagatttatcctgaattttaggaacca
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tcaaaacttcctacttacttcgtgcgttcggtaatcggtaacattagactttcaaaatca
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New isolated Borrelia burgdorferi nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X20251 standard; DNA; 53585 BP
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03-SEP-1997; US-0574
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                 Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
  therapy of
                                                                                                                                                                                                                                                                                         Gaps
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characterisation, prevention and t
isease. They can also be used for
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Best Local Similarity 46.9%
Matches 215; Conservative
                                                                                                                                              Lyme.disease
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Pred. No. 0.12;
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fragments
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Best Local Similarity 48.8%;
Matches 157; Conservative
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900001
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10
X20248_05
Continuation (6 of 10)
WP Sequence split into
WP Fragment Name
                                            X20248_01
X20248_02
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X20248_04
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X20248_06
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36325 TCTCTTTCTGTTTTGAATTTGCTTATAAATTTTTTTGTAACTTTCAGAAAAATTTAAAATT 36384

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125 aaattagaattttttttttatcaataaatattaatttattagttttattagaaatattaatt 184

65 tatctgtttattatgatttcagggcgcaaaaatgcgagtacttaataaaaattttacattt 124

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36385 TGATTTTTTTTTTCTTCTTTAAATATATATCCATGGATTTTGTTTTTTCATAATAAAAA 36444
                                                                                             36505 TTGTAAACTTACTTTTAATTTTAATATGATTAAAATTATAAGGGAGAATTTTTATGTA 36564
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X20248 to X20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs, to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetess are pathogenic in humans and Borrelia causes epidemic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi polynucleotide sequence #2.
Borrelia burgdorferi; splicochete; bacterium; pathogen; Lyme disease;
epidemic relapsing fever: endemic relapsing fever; Lyme borreliosis;
infection; diagnosis; characterisation; detection; ds
                                                                                                                                   185 agaaaattttgaatccccgatttctcctccttttcttcgctattcatcattttctaacca
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Pred. No. 0.12;
0; Mismatches 165; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO,
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22-JUL-1997; US-053377.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                       X20249 standard; DNA; 116277
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Matches 157; Conservative
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; US-050359
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W09858943-Al.
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Disclosure: F19 7: 108pp; English.

On open reading frame of 2349 bps extends from the 5' terminal end of the insert to a "TAA" stop codon. It is longest ORF found in the sequence.

Sequence displays some of the characteristics of other malaria nucleic acid sequence s: tandemly repeated motifs, high AT content and a cortesponding preference for codons containing these bases, and a high content of codons for glutamate. Three major repetitive sequences are:

Content of codons for glutamate. Three major sequences are:

Content of codons for putamate. Three major repetitive sequences are:

Content of codons for putamate. Three major pass to bp 411; another motif from bp 34 to bp 151 is repeated from bp 289 to bp 411; another motif from bp 567 to bp 611; a third motif from bp 1174 to bp 1233 is repeated tandemly 11 times. This last repetitious region consists of 360bp repeate differing only in 3 bases GAT coding for aspartate. This region is flanked to the 5' terminal od a degenerated 60 bp repeat. GC content coding part of the insert is on average 30%, and of the non-coding
                                                   18562 TIGIAAACTTACTTTTAATTTTAATATGATTAATAAATTATAAGGGAGAATTTTTATGTA 18503
                                                                                                                                                               18502 TAAAAATGGTTTTTTAAAAACTATTTGTCATTGTTTTTTAATTTTTTTAGTAATTGCTTG 18443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dziegiel M, Borre M, Jepsen S, Vuust J, Rieneck K, Wind A, Jakobsen PH;
WPI; 90-115998/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIATICAAGIIGIAAGIACAAIIAAAGGAAIAGCAAAGGAIATAGIAAIAII--IITCCA 2342
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Sequence encoding carboxylic terminal part of native GLURP.
Plasmodlum falciparum; antigen; malaria; vaccine; GLURP; ss
Plasmodlum falciparum.
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Pred. No. 0.17;
0; Mismatches 163;
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50.38;
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Matches 167; Conserv
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                                                                                                                protein of Plasmodium
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/note-"Alelle I."
3082. 3151
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091. .3120
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                                                                                                                                                         'note-"Sequence obscured
                                                                                                                                   Location/Qualifiers
                                                                                                              Sequence encoding the SERA protein
Malaria; SERA protein; vaccine; ds.
Plasmodium falciparum.
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DNA encoding SERA antigen of Plasmodium falciparum -
also DNA encoding signal and regulatory sequences of SERA gene,
for diagnosis, prevention and treatment of malaria.

Disclosure: p: English.
Sequence allows for production of antigenic malarial proteins, useful in
diagnosis, prevention and treatment of the disease. The sequence may be
used in an expression vector, and signal and regulatory sequences may be
used to stimulate production of other products.
Sequence 6124 BP; 2567.A; 602 C; 801 G; 2137 T; 17 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1484 TCTGATAATTCAAATGGATATAATAAATTAATTTTTTTTAACTCCTAGAAATATTTAAT 1543
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43.4%; Pred. No. 0.18;
tive 0; Mismatches 615; Indels
/*tag= t
/label=Complementary to Probe B.
/note="Alelle II, skips 3098. 3136.
485. 2526
/*tag= u
/label=Regulatory sequence.
                                                                                                                                                                                                 a (DAT2).

--AUG-1988; US-231771.

--AUG-1988; US-231771.

Inselburg JW, Bzik DJ;

WPI; 90-083508/11.

P-PSDB; R05526.

DNA encodir-
also-
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Best Local Similarity 43.4;
Matches 488; Conservative
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This list the nucleotide sequence of one strand of the PSI-PL470 gene of the 30.7 kb extrachromosomal plastid of Plasmodium berghel. This plastid encodes organelle-like rRNAS, tRNAS, tIbosomal proteins and RNA polymerase subunits, amongst others. Plasmodium is detected in a human or animal sample by treating it, or derived cortected in a human or animal sample by treating it, or derived cortected in a human or animal sample by treating it, or derived cortected in a human or animal sample by treating it, or derived cortected acid, (A) and detecting any hybridisation. (A) can include the PSI-PL470, PLH-PPH, PRB or PWO gene, the mitochondrial cort gene, and nucleic acids derived from them. Also new are to cort gene, and nucleic acids derived from them. Also new are used to diagnose Plasmodium infection. Also (not claimed) the polypeptides encoded by (A) are useful as targets for drug development and for development (A) from different species allows development of genus or species specific assays that result in
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  tatttttttttttgtaatttgacgaaccaaaaccagatttatcctgaatttaggaaccac
                                                1664 ITITITITITITITITITITITI------TIAACCGAATGAATAATATATTATGAGATCAC
                                                                                                                                            1716 AATTTTTAATAAT --- TTATTTTTTTTTTGGTTTAAATATTTTTTGTGTCACGATAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium berghei plastid PSI-PL470 gene.
Malatia; infection; therapy; diagnosis; vaccine; plastid;
PSI-PL470 gene; ds.
Plasmodium berghei ANKA strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kara AKU, Nelson JS, Tan TMC, Tham JM, Ting RCY; WPI; 98-447251/38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-1998; IB0212.
26-SEP-1997; AU-009481.
06-FEB-1997; AU-004953.
21-APR-1997; AU-006329.
(MOLE-) INST MOLECULAR & CELL BIOLOGY.
(UYSI-) UNIV SINGAPORE NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V33135 standard; DNA; 5849 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; glycophorin binding protein; inverse PCR; Plasmodium falciparum; malaria; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 1; Page 12-14; 17pp; German.

Claim 1; Page 12-14; 17pp; German.

Jycophorin binding protein 130h is a P.falciparum blood stage antigen 69% homologous with the known GBP130. The GBP130h gene and its homologues can be used in vaccines to protect against malaria caused by P.falciparum. The coding sequence was isolated using PCR techniques on a genomic P.falciparum FCBR strain library. The GBP130h gene was found to be highly conserved between different strains but is distinct from the GBP130 gene.
                                                                                                                                          886 atatctccttaccaatcatactaattattttgggttaaatattaatcattatttttaaga
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27-JAN-1992; 101271.
27-JAN-1992; DB-105348.
(BEHW ) BERRINGWERKE AG.
Hundt E, Knapp B, Kupper H, Nolte D, Kuepper H;
WPI; 92-286009/35.
Vaccines to control malaria
Length 5849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2418;
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Pred. No. 0.25;
0; Mismatches 343; Indels
                              Indels
                                                                                                                                                                                                                                                  1066 aagacacttattagacatagtcttgttctgtttacaaaagcattca 1111
                                                                                                                                                                                                                                                                               554 ITTACAAATITAAAATATATTCTTTAAAATTTTTAAATATGTTTAA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 G;
                             Mismatches 106;
 Score 56.4; DB Pred No. 0.23;
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Best Local Similarity 44.3%;
Matches 278; Conservative (
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/*tag= c
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Q27886/c
ID Q27886 standard; DNA; 2418
AC Q27886;
AC Q27886;
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/*tag- b
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                                Conservative
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                              Matches 120;
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1101 TAATTAGATATTTTAATAAATANTAAATATATTANACAGATATACTTAATTATTTAATT 1160

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ttattagaaatattaattagaaaattttgaatccccgatttctcctccttttttcttcgcta 1161 TTATTTTAAATATTAACTACNTAAGCTAGCANCTTTNCCTANATATATTATTATACTATA 227 ttcatcattttctaaccaaacca-----atcttatatgttcttcaaattagaact

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1281 TAAAACTNAATAATATTAAANAATAGTATTTATCTAACTATAACTTAAATCTTANTAATA 1340

tgaaattattaattataattaaactgaaaacaatttggtatcaattcatatacatgctta

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tgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattcatcatttaa 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aatatttttcaaatttgatagactattttttttttgtaatttgacgaaccaaaaccagat 699
                                                                                                                                                                                                                                                                                                                                                                                                          503 TATAAATTATCATATCCTTGAAAGAATATATGATATATTATTATAATTEGGTAAGTTACAAG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 ATAATATATATTTTTCCACATGTTCTTTTGTATCTATCTTTTCTATATAAATATA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example: Fig 13: 45pp. English.
A DNA sequence coding for a heterologous polypeptide which can be expressed in and secreted from filamentous fungi is claimed. Pref the DNA sequence codes for bovine preprochymosin, M. meihel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preprocarboxyl protease or A. niger preproglucoamylase. Also new are vectors consisting of the DNA sequence plus an operally-linked signal sequence. The vectors may also include a sequence which increases transformation efficiency, e.g. ANS-1. Sequence 1864 BP: 786 A; 210 C; 44 G; 732 T;
                                              caaaatttcatggcagcatgcctcagcccatgaaaaaaaccttataaaaatatctacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          820 ttgaccattgaaaagttcgttctcccatgggtaaccagatcaaactcacatccaaacata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 TCATTGATATTATTTTTTTTTGAATCTTAAAATTAAAAGAATTTAGAATATATTT
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WPI; 87-095049/14.
New DNA sequences for expressing polypeptide in filamentous fungi
- with secretion of prod. from the cells, and new vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enzyme; fungal expression vector; Aspergillus expression vector;
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Sequence of ANS-1 which increases transformation efficiency
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964 aagatttttaaaaaaatgtataaaattattattcatgattttcatacatttgattt 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base sequence coding RESA (N60472) or FIRA (N60473). RESA and FIRA have antigenicity suitable for providing protective immunity against blasmodium falciparum malarial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG:1991 (first entry) Sequence encoding the ring-infected Erythrocyte Surface Antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA coding for Plasmòdium falciparum antigens - expressing \mathrm{poly}:peptide(s) having antigenicity of RESA or FIRA antigens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anders R, Coppel RL, Brown G, Saint RB, Cowman AF;
                                                                                                                                                     Malaria vaccine; antigen; epitope; ss.
                                                                                                                                                                                               Location/Qualifiers
801. 995
                                           ВP
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                                           standard; DNA; 4590
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0-SEP-1985; AU-047326
                                                                                                                                                                             Plasmodium falciparum
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                                           N60472
RESULT 13
N60472
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3.6%; Score 56; DB 1; Length 1864; 49.1%; Pred. No. 0.27; ative 0; Mismatches 153; Indels

Query Match 3.6 Best Local Similarity 49.1 Matches 157; Conservative

tgttctgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatactaacagt 1148

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1444 TTAGTATTTTAATAATAAATCTTTTAAAAACTTCAAAACATTTTTGCATAAAATA 1503

ataaatatattttttttaatttcttaaaaaatgttgcaagacacttattagacatagtct

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1264 ATTATAATATGTAAATTATTAATAAATTATTTGTATAACATACAAGACTAAAGAAAAC 1323

1504 ATATTAATATTAGTAACCACCTAGATAAATTAGAGAAAACGTAGAACATACCAAAAAA 1563

22-NOV-1992 (first entry)
Sequence encoding the Histidine-rich protein (HisRP) associated with
the knob (K+) phenotype.
Malaria vaccine: Histidine-rich protein; cytoadherence; ss.

RESULT 15 025273/c ID 025273 standard; cDNA; 2104 BP.

Location/Qualifiers

Plasmodium lophurae.

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This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to This sequence represents the var-7 genes which have homology to the Duffy antiquen binding like (DBL) family of genes which have homology to the Duffy antiquen binding protein (DABB) and stalic acid binding protein (DABB) and T72888 respectively). The var family of genes modulate cytoadherence and antiquence variation of Plasmodium infected erythrocytes. SABP and the Duffy antiquen binding protein (DABP) are solubbe proteins that appear in the culture protein (DABP) are solubbe proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte surface. These proteins are necessary for erythrocyte invasion by the parasite. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and comprise either a nuclectide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to Plasmodium merozoites (especially
1024 tgataataabtatattttttttaatttcttaaaaaaatgttgcaagacacttattagacat 1083
                                                                                                                                                                                                                                                                                     Plasmodium var-7 gene.
DBL gene family; Shapp; stalic acid binding protein; vaccine; therapy;
Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
                                      1084 agtottgittotgittacaaaagcaitcaitcaitaaiacaitaaaaaataittaaiacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New malaria vaccines - contains cysteine-rich DBL family protein binding domains homologous domains of the Duffy and sialic acid binding proteins.
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/note= "no stop codon given"
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19124 BP; 7824 A; 2190 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES Chitnis C, Miller LH, Peterson DS, Si
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
7317. 15139
/*tag= a
                                                                                                                                                                                                                         T72882 standard; cDNA; 19124 BP
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16206. .17552
/*tag= c
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07-JUN-1996, U09508,
07-JUN-1995, US-4870
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P-PSDB; W22475.
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                                                                                                                                                                                                                                                                                                                                                                      Plasmodium; ss.
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47.2%; Pred. No. 0.29;
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Matches 164; Conservative

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Query Match Best Local Similarity

claim 1: Fig 4A-D; 29pp; English.

Two variants of HisRP are produced by P. falciparum. One is

Two variants of HisRP are produced by P. falciparum. One is

associated with what is referred to as "knobby phenotype" (K30) and

"knobless phenotype" (K-). The "knobby" and "knobless" phenotypes

have been implicated in cytoadherence, which is characteristic of

erythrocyte infection. It has now been found that CDNA expressing

both K+ and K- HisRP can be obtained by the use of P. lophurae HisRP

Histidine-rich protein associated with Plasmodium knob phenotype and DNA encoding it, used for in vitro diagnosis of $P.\,$

Falciparum infection

26-AUG-1986; 900401. 26-AUG-1986; US-900401. (SLOK) SLOAN KETTERING INST CANCER.

US5116965-A. 25-MAY-1992 Pologe L, Ravetch JV; WPI; 92-199590/24.

P-PSDB; R24392

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868 catccaaacataacatggatatctccttaccaatcatactaattattttgggttaaatat 927

1048 tttcttaaaaaatgttgcaagacacttattagacatagtttgttctgtttacaaaagca 1107

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210 ATCTTGTTTTCAGCAAAAATATCAFATAAAATATTTTTTTTATATATAAAAAA 151

1108 ttcatcatttaatacattaaaaaatatttaata 1140

Search completed: September 2, 2000, 02:07:29 Job time: 9218 sec

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AL034556 Plasmodiu
AL034556 Plasmodiu
AE001398 Plasmodiu
AC005083 Homo sapi
AL031746 Plasmodiu
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AL034559 Plasmodiu
AL09815 Plasmodiu
AC007465 Homo sapi
U11584 Drosophila
AC005504 Plasmodiu
AC004157 Plasmodiu
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J01462 Yeast (S.ce
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4 161286 67 AC025120 4 173915 9 AP001254 4 1897 8 SCU32857 4 3542 7 YSCMTGG16 4 157781 55 AC011355 4 175516 0 AC010280 4 34996 34 U87145 3 163678 52 AC010178	91.6 5.2 2226 33 MIDYTRN 81.6 5.2 75076 39 AC004948 81.2 5.2 75076 39 AC004948 81.8 5.1 14867 34 AE001398 80.8 5.1 1460 34 AF51382 80.4 5.1 146285 39 AC005083	80.2 5.1 110000 31 80 5.1 9434 39 79.6 5.1 161894 55 79.6 5.1 193561 39 79.4 5.0 170109 39	ALIGNMENTS	T Z.	9 9 G 4 G		JOURNAL MOI. BIOL. EVOI. 11, 523-538 (1994) MEDLINE 94285822 REFERENCE 2 (bases 1 to 4601) AUTHORS Kaquni,L.S. TITLE Direct Submission JOURNAL Submitted (28-JUN-1994) Laurie S. Kaquni Ph.D, Dept. of	Blochemistry, Michigan State University, East Lansing, MI, 48824-1318, USA Location/Qualifiers Source 1.4601	/organelle="mitochondrion" /strain="Oregon-R" /db_xref="taxon:7227" /dbu strane="mhrvo"	gene 1. 4601 /gene="mt.ori" /note="mitochondrial origin"	/db_xref="FlyBase:FBgn0013687" repeat_unit 6501022 /gene="mir.ori" /note="Peneat'ra"	/db_xref="FlyBase:FBgn0013687" /rpt_type=tandem repeat_unit 1033. 1360 /gene="mt:ori"	/note="repeat I-B1" /db_xref="FlyBase:FBgn0013687" /rpt_type=tandem repeat_unit 1361. 1705

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48.4%; Pred. No. 1.2e-06;
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Drosophila melanogaster mitochondrial DNA, a novel organization and
Transfer RNA genes in Drosophila mitochondrial DNA: related 5' flanking sequences and comparisons to mammalian mitochondrial tRNA
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                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster mitochondrial DNA: gene organization and evolutionary considerations
Genetics 118 (4), 649-663 (1988)
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                                                                                                                                                                                                                                    (bases 804 to 1778)
Satta,Y., Ishiwa,H. and Chigusa,S.I.
Analysis of nucleotide substitutions of mitochondrial DNAs
Drosophila melanogaster and its sibling species
MOI. Biol. Evol. 4 (6), 638-650 (1987)
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Satta,Y. and Takahata,N.
Evolution of Drosophila mitochondrial DNA and the history
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Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9558-9562 (1990)
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Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Drosophila melanogaster mitochondrial DNA: comple
nucleotide sequence and evolutionary comparisons
INSECT MOI. Biol. 4 (4), 263-278 (1995)
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Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Direct Submission
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Science 258 (5086), 1345-1348 (1992)
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Drosophila melanogaster complete mitochondrial genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         taaaacaaaatttcatggcagcatgcctcagcccatgaaaaaaaccttataaaaatatct
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Clary, D.O., Wahleithner, J.A. and Wolstenholme, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila mítochondrial DNA: a novel gene o
Nucleic Acids Res. 10 (21), 6619-6637 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion Drosophila melanogaster
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LSLALPLWLCFWLYGWINHTQHWFAHLVPQGTPAILMPFMVCIETISNIIRPGTLAVR
LTANWIAGHLLLTLLGNTGSSMSYMLMTFLLMAQIALLVLESAVAMIQSYVFAVLSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Lranslation="MSTHSNHPFHLVDYSPWPLTGAIGAMTTVSGMVKWFHQYDISLF
VLGNIIIILTVYQWWRDVSREGTYGGLHTYAVTIGLRWGMILFILSEVLFFVSFFWAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQGLFFTVLLGIYFTILQAYEVIEAPFTIADSIYGSTFFMATGFHGIHVLIGTTFLLV
CLLRHLNNHFSKNHHFGFEAAAWYWHFVDVVWLFLYITIYWWGG"
                                                                                                                      'translation = "MPQMAPISWLLLFIIFSITFILFCSINYYSYMPNSPKSNELKNI
                                                                                                                                                                                                                                                                                                                                              /translation-"MMTNLFSVFDPLAIFNFSLNWLSTFLGLLMIPSIYWLMPSRYNI
                                                                                                                                                                                                                                                                                                                                                               MANSILLTLHKEFKTLLGPSGHNGSTFIFISLFSLILFNNFMGLFPYIFTSTSHLTLT
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Pred. No. 8.2e-07;
0; Mismatches 531;
                 db_xref-"FlyBase:FBgn0013685"
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                                                                                                                                                                                                                                                                                                 /protein_id-"AAC47815.1"
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                                                                                                                                                                                                                                                                                                                         /db_xref-"GI:1166534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"G1:1166535
                                                            /product-"ATPase 8"
                                                                                                                                                                                                                                                                               /product="ATPase 6"
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                                          /transl_table=5
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/gene="mt:ND6"
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                                                                                                                                                                   4062. .4736
/gene="mt:ND6"
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ilarity 48.4%;
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                                                                                                                                                                                                                                           "un_xret= c1:1100330"
'translation="MFNNSSKILFITIMIIGTLITVTSNSWLGAWMGLEINLLSFIPL
                                                                                                                                                                                                                                                                                                                       GAIGGLNQTSLRKLMAFSSINHLGWMLSSLMISESIWLILFFFYSFVLTFFFNIF
KLFHLNQLFSWFVNSKILKFTLFMNFLSLGGLPPFLGFLPKWLVIQQLTLCNQYFMLT
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VSTIGSTISLLGILFFFFIIWESLVSQRQVIYPIQLNSSIEWYQNTPPAEHSYSELP
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HSWTVPALGVKVDGTPGRLNQTNFFINRPGLFYGQCSEICGANHSFMPIVIESVPVNY
                                                                                                                                                                                                                                                                          LSDNNNLMSTEASLKYFLTQVLASTVLLFSSILLMLKNNMNNEINESFTSMIIMSALL
                                                                                                                                                                                                                                                                                                   LKSGAAPFHFWFPNMMEGLTWMNALMLMTWQKIAPLMLISYLNIKYLLLISVILSVII
                                                                                                                                                                                                                                                                                                                                                               IMMMSTLITLFFYLRICYSAFMMNYFENNWIMKMNMNSINYNMYMIMTFFSIFGLFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="cytochrome c oxidase subunit.I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_except=(pos:3767,aa:TERM)
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complement(1322. .1383)
/product="tRNA-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | sene="mt:ND6"
| product="tRNA-Leu"
| p. xref="flyBase:FBgn0013685"
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3907. .4068
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join(1470. .1472,1474. :3009)
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                                                                                                                                                                                                                                    /db_xref-"GI:1166530'
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/gene="mt:ND6"
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/gene="MAL3P5.2"
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Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S.; Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassall, B., Kyes, S., McLean, J., Murph, L., Oliver, K., Quail, M.A., Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S., Sulston, J. E., Whitehead, S., Woodward, J.R., Newbold, C. and
                                                                                                                                                                                                                                                                                     17998 ATTTTTAAAAATTTCTTAAATGTATTATTTTTATAAAAATATTTATATAATAAAAATCA 18057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18058 TGTTTTTAAAAATAAACAAAAATTTTTAATAAATAAATTTTATAATGAAATATAATT 18117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            איני., Squares,S.,
Newbold,C. and
                                                                                                                      1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum MAL3P5, complete sequence.
AL014556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179
AL034556.2 GI:4493931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       he complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                               tectgaattttaggaaceae----agatgtaaetaaaceaatatttatttte 754
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 86829)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T.,
Churcher,C.M., Craig,A., Davies,R.M. Devlin,K., Feltwell,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowman, S., Skelton, J., Churcher, C., Lawson, D., Quail, M. and
                                                                                                                                                                                17698 TTTTTTTTAAAAAAACTATATACTAATTATAAATTAATAGAÇATTTATATATATAT
583 cattagactttcaaaatcatttttaacccctaaacagtaaatttgaaggacaaaaataat
                                    taaaacaaaatttcatggcagcatgcctcagcccatgaaaaaaaccttataaaaatatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --tttcttaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaag
                                                                               643 atttttcaaatttgatagactattttttttttgtaatttgacgaaccaaaaccagattta
                                                                                                                                                                                                                                                                                                                              acacattgaccattgaaaagttcgttctcccatgggtaaccagatcaaactcacatccaa
                                                                                                                                                                                                                                                                                                                                                                                                                  acataacatggatatctccttaccaatcatactaattattttgggttaaatattaatcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tatttttaagatattaattaagaaattaaaagatt--ttttaaaaaatgtataaaaatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1106 cattcatcatttaatacattaaaaaatatttaatactaacagtagaatcttctt 1159
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Barrell, B.G.
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The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
On Mar 24, 1999 this sequence version replaced gi:4034877.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
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IEGADIEFQNFLSNVNLDOHGRVKSNDENTKSTEHIKNKNTINKGYDTELIQNOMENN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MYLKNVYIYISSCFILFDLCFSFHLLKMKYKNHMNNMKSVTFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSPQIYRKRFKRSRIKNVSFKKKQKKPLFLFENLKKGFSFLGFWRNQYDQVNKREKKP
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Hypothetical protein, len: 1828 aa"
/codon_start=1
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Hypothetical protein, len: 1097 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(324. .668,1199. .1303,1460. .2944)
/gene="MAL3P5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein, len: 645 aa"
                                                                                                                                                                                                                                                                                                    /organism-"Plasmodium falciparum"
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/gene="MAL3P5.2"
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                                                                                                         GEIWRLFTPYLYIGNLYLOYILMFNYLNIYMSSVEISHYKKPEDFLIFLTFGYISNLL
FTIMMAMYNENIMNYKLYIHPRNFFIKDCVSKTYRSSSTWINNSNNINSKNINSSNNIN
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YNKEIFNFSILKFENHLNNVNINLHSLSLFFYSYSVYFINNCFYYYYYFHSFFNITTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INIYVNINKIYLNDEEENTSHCIKIKNDNKKDILYHDHMKFLYNLMNEIIYRNDLLN
MKOIILLLYGLKFNNFMFLOFEKIILKRFICLPKKEIOKIGKEEIMFLYQYFFVRTCL
FNELKKQNNLFISQDEYENYIYISDKYNESAKLDNSYNMPSNLKEKNTNHHGGKDNTL
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                                                                                                                                                                                                                                                                                                                                                     FINIINKNLHLYNSTDLMFLYIGSLHIHNMYTPNHVDONKEPKNNOKENNNYHNDNHN
                                                                                                                                                                                                                                                                                                                                                                                IYLKNINNNCYDHRLDSNDFITMTNYDQGEYNKHIQQNKHIQQNKHIQQNKHIQQNKH
                                                                                                                                                                                                                                                                                                                                                                                                        IQRIGTHCTESNSNNQQLIQIQNDEKENKLITYDNSKHNLLKDPCQHNIVEKDGEKKQ
NLIKNLIINIKKIIEEKLSSFKIQEIVNILFVSLNKNIIINKKYFHFLNQEKINIRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLY IHDDLFYMNKNKKRDRYKIYLYDNFIFNYPAYYVEQKKDHIDYNESVNNFDNMKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIQLKKKK INKINNNNNNNNNNNIY IDTNIQTVNKNYSCTHNNVIKNETNDNYPNS
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SIKPPVIICGDIHGQFFDLLELFDVGGDIMNNDYIFLGDYVDRGYNSVETFEYLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLFPKNITLLRGNHESRQITTVYGFYDECFKKYGNANAWKYCTDIFDYLTLAALVDNQ
IFCVHGGLSPBIKLIDQLRLINRVQBIPHEGAFGDIMWSDPDEVDDWVANPRGAGWLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPNVTKKFNHINNLELIARAHQLAMEGYRYMFEDSTIITVWSAPNYCYRCGNVAAIMR
IDEYMNRQMLIFKDTPDSRNSIKNKATIPYFL"
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27547. .28290
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KKDEPESTISTLKKNMTKNEDSDNNYNNFYDENGEKKTTTNYCNDHINLPIDEEKELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹.
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                                                                                                                                                                                                                                                                                                                                                               /note="predicted using hexExon; MAL3P5.8 (PFC0610c), Hypothetical protein, len: 1182 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atttttaacccctaaacagtaaatttgaaggacaaaaataatattttcaaatttgatag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agaaaattttgaatccccgatttctcctccttttcttcgctattcatcattttctaacca
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15.4%; Pred. No. 0.00011;
ve 0; Mismatches 617;
248
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protein, len:
                                                                                                 /db_xref-"SPTREMBL:Q9Y011"
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                                                                                                                                                                                                                                                         CBIO ISA, UK
On Mar 24, 1999 this sequence version replaced gi:4034877.
For more information about this sequence or the Malaria Project,
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AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL0109179
AL034556.2 GI:4493931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete nucleotide sequence of chromosome 3 of Plasmodium
661 actatititititigiaatitigacgaaccaaaaccagatitatccigaatittaggaacc 720
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1 (bases 1 to 86829)
Bowman, D., Lawson, D., Basham, D., Brown, D., Chillingworth, T.,
Churcher, C.M., Crabig, A., Davies, R. M., Devlin, K., Feltwell, T.,
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Bowman, S., Skelton, J., Churcher, C., Lawson, D., Quail, M. and
                                                                      acagatgtaactaaaccaatatttattttattttctaaaacaaaatttcatggcagcatgc
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99376085
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FFCFFLCYNILERIYEECVGDLIRKKIERYNLYCEKKKIKFHMKDAIKKMEINMKDDD
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DQKKDILKKIYFLKGNKLDDIQILNELYVMIYMRLLFECSLKLISIKKNIHLLEKKME
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YSYDTMVNSFTFSYFFFSLSYLLFILFYHPDMYASYIFFKTLTYSGLPTYYYSLYNNI
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KNKLKEYYEKIKNHVIKKKKKIFSLKFSQNKRNEKKKKYFFINFTSFHDIKDNIKVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSPQIYRKRFKRSRIKNVSFKKKQKKPLFLFENLKKGFSFLGFWRNQYDQVNKREKKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKFKYQYDIINEQYPIIKNEKTVLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLGLKRKNVFYLLVSVPSLFAYFLKRHKDNENNYETLINNNDIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAL3P5.2 (PFC0580c),
aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using hexexon; MAL3P5.4 (PFC0590c), Hypothetical protein, len: 1828 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted using hexExon; MAL3P5.1 (PFC0575w),
Hypothetical protein, len: 645 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MAL3P5.4"
complement(join(13655, .17801,18019, .19355))
/gene="MAL3P5.4"
see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         Juin(324. .668,1199. .1303,1460. .2944)
//gene="MAL3P5.1"
                                                                                                   /organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="predicted using hexExon; Hypothetical protein, len: 1097 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:097258"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB38968.1"
/db_xref="GI:4493932"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB38969.1"
/db_xref="GI:4493933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="MAL3P5.2"
/note=""A
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/gene="MAL3P5.2"
                                                                                                                                         /strain="3D7"
/db_xref="taxon:5833"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                                     /gene="MAL3P5.1"
                                                                                                                                                                                                                                                    /clone="MAL3P5"
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HYNNSKHIDIKKEQYNHLGYVESTYILYYWSRINEGTLINCFELFTRAEYVPPFFIT
ONLLLYNESELYEVASIFSSYLFFTYEKYFKRYLEFKTLLKVIHTYPLYDRFODM
TKLLISILKKRNGPLPFLORCYTHWPRINTWRHMISDLRKNIEVORKNVKHVKNV
WSNFLYIILKLFRENEKNYVDFMILKLLSKYIKIEKKYLLYICEOLEHETYKFRTR
DLTLLILIRRNNFDNIYYINLISKSILMYMRNMSYKDLALITYSLSKNIYLTDEQI
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NKRIKYIKDKSLLAINHKTKNIIEKQKISTSNHLSKLKRMFSL"
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SIKPPVIICGDIHGQFFDLLELFDVGGDIMNNDYIFLGDYVDRGYNSVETFEYLLLK
LLFPKNITLLRGNHESRQITTVYGFYDECFKKYGNANAWKYCTDIFDYLTLAALVDNQ
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GPNVTKKFNHINNLELIARAHQLAMEGYRYMFEDSTIITVWSAPNYCYRCGNVAAIMR
IDEYMNRQMLIFKDTPDSRNSIKNKATIPYFL"
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SCHYTIKKLKTCRPDADIRLLEKHLAFRONTLIKNIQEERKKGIGINGNESES
NSSSSNYDNYLLYRKINRLNKTNYKKSKNRSKRKRINSKIDKKYIIKCRACKFINP
NGFKIEDYYTCQNCGYNDFSVIRSTSPNNAD
                                                                                                                                                                                                                                                                                                                                                                                                    YNKEIFWFSILKFENHLNNVNINLHSLSLFFYSYSYYFINNCFYYYYYFHSFFNIITK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLY I HDDLFYMNKNKKRDRYK I YLYDNF I FNY PAYYVEQKKDH I DYNESVNNFDNMKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIQLKKKKINKINNNNNNNNNNNIYIDTNIQTVNKNYSCTHNNVIKNETNDNYPNS
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NHKLSCLQSIDILCIYEKLNIRDYRIIKYLYNLKKELLYLDNTYLLKVINIIVKFNLY
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LFKNLYNLQNIQDLKKIEMMNYDNLTFKFYKLFKNILSINVKRYVQNCNSYNKYEMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THTNNLNKNEQHKY IHHNNDHKDGRHNNNNNHYDKVDVSSSSSSSYYYYLNKSGKNLG
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FT I WANMY NEN I MNVKLY I HNFKNFFIKDCVSKYTSRSSTNNNSNN I NSNNRSSNN NN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKOIILLLYGLKFNNFMFLQFEKIILKRFICLPKKEIQKIGKEEIMFLYQYFFVRTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NINVQNLDDININKIKSISYKIKKDQIKDIGYMRVSKYSELMKSMKMMNYDEHFNDEY
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Hypothetical protein, len: 250 aa"
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Hypothetical protein, len: 248 aa"
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complement(20528. .21454)
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27547. 28200
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/db_xref="SPTREMBL:Q9Y011"
/translation="MGGHGGLNILPQKKWNYYRKDAQYKVHYDEHKIIKEEKDKEIKR
                                  KKDEPESTISTLKKNMTKNEDSDNNYNNFYDENGEKKTTTNYCNDHINLFIDEEKELT
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                                                                                                                                                                                                                                                                                                                               DNELKQIKEFHDISNENEHNENRSFSTSTLSSFFKEYEENSVEQHFFSEGTHTEHSME
DSNNVETIENAITNDVLRSNRSTSYSKQKNELTSVTCYVGGETVDLNIMSDHIFAHKL
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                                                                                                                                                                                    /note="predicted using hexExon; MAL3P5.8 (PFC0610c),
Hypothetical protein, len: 1182 aa"
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Pred. No. 0.00017;
                                                                                            HIKKIIKYKQEKDKEKKRKRGGKEKKKPK
                                                                                                                                                 complement(29992. .33537)
                                                                                                            complement(29992. .33537)
                                                                                                                                                                                                                                    /protein_id="CAB38971.1"
/db_xref="GI:4493935"
                                                                                                                                                                  /gene="MAL3P5.8"
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SSIFSKKRDSHKKGSSFRGRRSGFINRKSGSFKKPYYNNRLINKNYNNYKGRNFHNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         malaria parasite P. falciparum.
Plasmodium falciparum
Plasmodium falciparum
Plasmodium falciparum
Labraryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 14867)
Gardner, M.J. Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, I. Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J., Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.; Smith, H.O., Fraser, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L. Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02 NOV-1998) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
                             1079 gacatagictigiticigitiacaaaagcaitcaicattiaatacaitaaaaaaataittaa 1138
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ctcagcccatgaaaaaaaccttataaaaatatctacacattgaccattgaaaagttcgtt
                                                                                                                                                                                                                       gattttgataataaatatattttttttaatttcitaaaaaaatgttgcaagacacttatta
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                                                                841 ctcccatgggtaaccagatcaaactcacatccaaacataacatggatatctccttaccaa
                                                                                                                                     Erratum: [[published erratum appears in Science 1998 Dec 4;282(5395):1827]]
2 (bases 1 to 14867)
Gardner, M.J.
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/db_xref="taxon:5833"
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/protein_id="AAC71887.1"
/db_xref="GI:3845198"
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GLKKGSLKSKTRKSTSGSKFKPLNKYFLSKIKIVTSLNKIPSPLKEQKNTEVNLPESL
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Pred. No. 0.00037;
                                                                                                                                                                                                                                                                                                        /product-"hypothetical protein"
/protein_id-"AAC71888.1"
/db_xref-"GI:3845199"
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/gene="PFB0495w"
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Best Local Similarity
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Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 12, 1999 this sequence version replaced 91:3212908.
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Park Avenue, St. Louis, Missouri 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Homo sapiens BAC clone CTA-281G5 from 7pi5-p21, complete sequence.
ACOO5083
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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( bases 1 to 146285)
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l (bases 1 to 146285)
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone CTA-281G5 is from a release of the human BAC library CITB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                             all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
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Actual start of this clone is at base position 1 of CTA-281G5;
actual end is at 146285 of CTA-281G5
                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTA-281G5 contains an E. coli transposon from 10982 t is not represented in the submitted sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     sequence was finished as follows unless otherwise
                                                                           rpt_family="purine-rich"
891. .7126
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/clone="CTA-281G5"
/clone_lib="CITB-HS-A"
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882. .2171
rpt_family="Alu"
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rpt_family="AT_rich"
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rpt_family="AT_rich"
764. .6034
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'rpt_family="L1"
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L_family="(CAAAA)n"
35. .22857
L_family="MER4-group?"
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family="MER1_type'
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02. .12110
                                                                                                                                                                                                                                                                                                                                                 family " (CAATA)n"
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.13367
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6130, .26254
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pt_family="(CA)n"
56. .8533
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5826. .25846
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                    t_family="L1"
5. .7481
rpt_family="L1"
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11101 ATTTATATACAATATATATATTTATTATGTATAATA-----CAATATATATATTA 11050
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Pred, No. 0.00077;
0; Mismatches 569;
                                                                                                                                                                                                                                                                                                                                   18124, .38899.
/rpt_family="Retroviral"
                                                                                                                                                                                                                                "(CATTT)
                                                                                                                                                                                                   ly-"AT_rich"
rpt_family="AT_rich" 6792. 27716
                                                                                                                                                                                                                                                            t_family="(CA)n"
24 .36007
t_family="L2"
                                                                                                                                                                    Ly-"MIR"
                                             pt family-"Alu"
                                                                        t_family="MIR'
                                                                                                                                                                                                                                                                                                                           y="L1"
                                                                                    rpt_familv="r"
                                                                                                                       32448
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Best Local Similarity 44.5%;
Matches 467; Conservative
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complement(1748..3276)

/gene="MALIP3.01"

/gene="MALIP3.01"

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/no
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Submitted (24-SEP-1998) P. falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Dec 16, 1999 this sequence version replaced gi:5763807.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P-falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein, UPP0006 family"
/protein_id="CAB63556.1"
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                                                           10749 ITGATATATTTATATATATATATATGATGATTATTCATATATTTATATAATACAATAT 10690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gatattaattaagaaattaaaaagattttttaaaaaaatgtataaaaattatattcatg 1003
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                                                                                                                                                                                                                                                                                                                                                     943
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769 atggcagcatgcctcagcccatgaaaaaaccttataaaaatatctacacattgaccatt
                                                                                                                                                                                                                                                     10869 TATAATATATATATATTATATATATATATATATAGATATATATATATATATAT
                                                                                                                                                                        gaaaagttcgttctcccatgggtaaccagatcaaactcacatccaaacataacatggata
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Plasmodium falciparum MAL1P3, complete sequence.
AL031746
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/strain="3D7"
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1 (bases 1 to 67970)
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Plasmodium falciparum
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JOURNAL
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REFERENCE AUTHORS

COMMENT

RESULT PFMAL1P3

LOCUS

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FEATURES

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NEKDK EYLENLKNKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
CSLKSLENINAVKKIPLNLLLLETDAPWGGVKKTHASYEYIKDTYEKRAYTNLKKIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEERKYSQTDLFR
KKOEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKOSLIDIIQS
translation-"MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
                                        JOIKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKMFDGVYNSKKHENDLQNVLNRAK
                                                                        NNNVDKIIITCTCLAEIDKSLKICETYDPEGKFLYLSAGVHPTNCYEFIDKNKHEEKE
                                                                                                                I I AKK EY EEFIKY FKNEQVENSKMENGNKKICDGEKDMNNLNEILLEKNLDTIPGFKY
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translation="MKLLNNRFVVLCPIIILFFFLNSVVLGNNNRNNINFHETENAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3DIQELPNICRNFDVPYYASKLEENLRDIEVEDSEFYSEKNSSNEHVLHHCNSNDASE
KKVYNVYYHNILMSILKTFKFRIILIISFYILETLIVTLGGKFIDYYMRILEGQKIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISFLKDFKVFSGLVVVMIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RALY EHY IHMHKLCTDY EKKLIQPNEILDKDLINNKNISSYNNKKSKLVNYNIPFNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKEHMNKNNKDNNNNNNNNNKDDHININMNDNHRNYNDINLGPNSTDDSPTVSSLGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MTTYKENVGISNKGNKKKKSCQNISFLNFLSFDWIRPLINDLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHLQNPDAFYNTYRKFSSQTEIDEISRDFLSIGKNASSSSSGIKNNNKNIDNNKFVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKMEKDSLNENRSLPNVNIYNIMFSDVPSVTFFVTSCINLFNVFVKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYYNDIKNY FMYRTRYNEDYNIVVDKTFLQNENIT SHDDGTSHNLKHLKNV I KNKLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MFKY FFFY HKMNY HKNI INKQ ILSGLLK NVDDNT NKK ICFQ EHKSNSTY NY NSSH IHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIRSMILFGNEYNPLIYKYTILQSELLNDLSTIEHGDMKYINDDHNLSKGOKVRICLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        !LDNFLIEDILDNVQYEVNIEEIQDKTLKYRGNISEYMEKNNLNITKESHWGYSNLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDYTRIKLFDEVELNHVKHSNKMIYKEAYFVKGNTESVSFEIDSINKEYIKKMKKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLDTYTSNNSDKEEIVKPLYKDTHEEFNKSSSMPFVKSSSNMINNPSNFKYEDNSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSFYVFHIKIGSNSVGIAIWLSIALYSAMILFEFLPSLFKSKYLIYRDKRIDNMHHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y LKDRLNKKEE IKFTSI I MPLY VYKI LISNVANFPNLVNNVMEGI VNIKRLNNY I NDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTDEIKFVFLTMMSIISKNNKEHSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGICFSMIIYGNITSAIKVHNNILYSILNAPLYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL
NVITTQTYKEKNENISDKISAIVEYKNVSLSSIINSSQDDESKKKYGIKFENVYVSYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLTTY I IMHPHLYASGI IKLYKEKNYVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MAL1P3 03, putative ABC transporter, len: 1822 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="possible cen1, region of very high [A+T] content"
14884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"MALIP3.02, hypothetical protein, len: 163 aa,
contains possible signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence, atg/gttaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="potential splice donor sequence, aaa/gtaaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="hypothetical protein, MALIP3.02"
protein_id="CAB63557.1"
                                                                                                                                                                                                                                                                                                                                                                                /note-"potential splice acceptor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acceptor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="putative ABC transporter"
protein_id="CAB63558.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HY INNFRISYFFKWLINIWASLY IKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="potential splice dcomplement(2849. 2861)
/gene="MALLP3.01"
/note="potential splice accomplement(2984. 2989)
/gene="MALLP3.01"
                                                                                                                                                                                                                                                                                                /gene="MAL1P3.01"
/note="mal1P3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                complement(2742. .2747)
/gene="MAL1P3.01"
                                                                                                                                                                                                                                                                IIKCDDNTIFKERNEPYNIA complement (2599. .2610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="GI:6594246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     005. 5496
gene="MAL1P3.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         005. .5496
/qene="MAL1P3.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="MAL1P3.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="MAL1P3.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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/translation="MKKSYTFINVTILLFLTYTYLYDTFSKTKFNNNIKIDIN
RFKRIIAEASEEGKYPWEEDFCLILNEELIRPEHNDSPYLPEHYENIDKINELSINS
TKIWKETIKKHRONYEKETDAMNHNRRDFMHYKMANIYLYKVHKLINITLKDLTNPI
HDKETITTHIKHNIDELEYFLFNLQVEWLRILTLELFYKNKE"
COMPLEMENT (32477). 32486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation-"mrikmnsgiffikllicisficvfecfnkcmisyrkdllwysen
Frysidrslaegssesketkvkdipniellkslninyeeyekmkelvgsfmdnnnln
Anevlknihsftnienifslindsskspylktfekefgsifphmlnnypkllfblcq
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Journal MALLES 104, conserved hypothetical membrane protein, en: 203 da. similarity: P. falciparum chromosome 2, FEB0110W, 096126 predicted integral membrane protein (255 a), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity in 191 aa overlap).
                          KITVEGRDIRTYNRKGEDSIIGILAQSSFVFYNWIRTFIDPYNNFTDDEIVHALKLN
GINLGKNDLYKYMHKQDMKSNYKKIIOTSKVINQSNDNTILLINDCIRYLSLVRLYLN
RHKYKIILIDEIPIFNLNNSVHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGGCCIISSVHETSNDTKDNDKENISEDKKEDHQQEEMLKTLDKKERKQKEKEMKEQE
KIEKKKKKQEEKEKKKQEKERKKQEKKERKQKEKEKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation-"MNVLFLSYNICILFFVVCTLNFSTKCFSNGLLKNQNILNKSFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGRLLNETELEKNKDDNSKSETLLKEEKDEKDDVPTTSNDNLKNAHNNNEISSSTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'NI I NVNDKDNENSVDKKKOKKEKKHKKOKKEKKEKKDKKEKKDKKEKKHKKEKKHKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HDKENEETMQQPDQTSEETNNEIMVPLPSPLTDVTTPEEHKEGEHKEEEHKEGEHKEG
(KIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : almost
97.6%
                                                                                                                                                                                                                     5.8S and large
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="potential splice donor sequence, aaa/gtatat"
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36854. .36863
/gene="MALIP3.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product-"conserved hypothetical membrane protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //octe="MALLP3.06, garp, len: 673 aa, similarity:
identical to GARP_PLAFF (678 aa), fasta scores: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="MAL1P3.05, hypothetical protein, len: 188
                                                                                                                                                                                                                                                                                                                            complement(31966. .32775) % Complement(31966. .32775) complement(join(31966. .32476,32675. .32775)) /gene="MALIP3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(38049. .39995,40210. .40284))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product-"hypothetical protein, MALIP3.05"
'protein_id="cAB63560.1"
'db_xref="GI:6594248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="potential splice acceptor sequence"
complement(32669, .32674)
/gene="MALIP3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="potential splice acceptor sequence"
complement(38049. .40284)
                                                                                                                                                                                          //occe="region containing small subunit,
subunit rRNA genes and spacer regions"
23896. 31533
/gene="rRNA"
                                                                                                                       LSCCDYIYVLRKGEITYRCSYEDVKTQSELSHLLEMDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="hypothetical garp protein"
protein_id="CAB63561.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .37343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNPLHIILGLIVILAAIYVFENFKNFEC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MAL1P3.05"
|oin(36657. .36743,36864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identity in 678 aa overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_id-"CAB63559.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref-"GI:6594247"
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/gene="MAL1P3.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="MAL1P3.05"
                                                                                                                                               23896. .31533
/gene="rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 691
                                                                                                                                                                                                                                   splice donor sequence, aag/gtaaca"
                                       DODAEEDDDDAEEDDDEDEDEDEEEEEEEEEKKIKRNLRKNAKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTTATATTATATTAAATTAAATATATATAAATTAAATAAATTAATAATTAATAAATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATAATAATAAATAAAATTAAAATTATTAAATTAATTAAATAATAATAATAATTAATTA
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                                                                                                                                                                                                                                                                                                                                                    212 teettttettegetatteateattttetaaceaaaceaatettatatatgttetteaaatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTAAAATATATAATTAATAATTAATTAAAATATTATTAAATGAATTAAATGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAAATAATATATATAAATTAAAATTAATAAA - TAAAATAATAATAATTAAATTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAATAAATAAATAAAATATT - - ATATTAATTTATATGTTTAATATATTGTCTTTATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tetacacattgaccattgaaaagttcgttctcccatgggtaaccagatcaaactcacatc
                                                                                                                                                                                                                                                                                            attaatttattagttttattagaaatattaattagaaaattttgaatccccgatttctcc
                                                                                                                                                                                                                                                                                                                                                                                                          gaacttgaaattattaattataattaaactgaaaaacaatttggtatcaattcatatacat
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                                                                                                                                                                                                      17;
                                                                                                                                                                             Length 67970;
                                                                   /gene="garp"
/note="potential splice acceptor sequence"
complement(40204, 40209)
                                                                                                                                                                                                         Indels
                                                                                                                                                                             DB 33;
                                                                                                                                                                             Score 91.8; DB 33;
Pred. No. 0.0012;
0; Mismatches 547;
                                                       complement(39996. .40005)
                                                                                                            /gene="garp"
/note="potential
45401, 50233
                                                                                                                                                     /gene-"MAL1P3.07"
                                                                                                                                                                             5.8%;
larity 46.3%;
Conservative (
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/gene="PFC0175w"
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NKYNDILINLEYOKLSLYSOVSOERINSLDEDYRNAILYNONPRVKSNHKYLYISTVL
HIYIYIYIPFFFFFFELEYLCDLOYYKTSKGSSLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MNDNESLDSEVLEKQYEIIKYAKYQDFIRLQILIQPYLLNNDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCFGISILFHKNRRRASPFLTAICEFNEDKILEALHILELLYMNGVSLEEQNEHGGTA
LFLSVKKNNISTLQMLLTKEVNINHRDFYGNTVLHIAVRHCDIDILKLLCDYGCLNMV
YYSSIENKNTNVFQLCIKNRYFLVYILLKKWVLQNKICSKLKICKTIYAFYFWFFAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nlivyfniahsfsiinkyhfksliwitiwffqqflwcmlyfkspgfykenhmfnknkk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Mar 24, 1999 this sequence version replaced gi:4034874.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is not the entire insert of clone MAL3P2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLNSINILHWACYCGFTELVKKLISFNCDIEKEDLVNNDTPIYYAIKNSNYEIVLLL
                                                                                                                                                                                        1052 traaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattca 1111
                                                                                                                                                                                                                     FEMALSP2 153098 bp DNA INV 28-JUL-1999 Plasmodium falciparum MAL3P2, complete sequence. ALO184558 ALO08982 ALO08989 ALO08007 ALO09008 ALO090014 ALO10150 ALO10158 ALO10211 ALO22217 297350 298546 ALO184558.2 GI:4493878
932 cattatttttaagatattaattaagaaattaaagatt 991
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Putative Ankyrin repeat protein, len: 285 aa"
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Churcher, C., Bowman, S., Lawson, D., Quail, M. and Barrell, B. Unpublished
                                                                                                                                         /organism="Plasmodium falciparum"/strain="3D7"
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/gene="PFC0165w"
join(5344. .12004,12737. .13329)
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                                                                                                                                                                                                                                                                              'protein_id="CAB38988.1"
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1. .153098
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/gene="PFC0160w"
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/gene="PFC0160w"
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SLRDKANNNQLDKSDITNGTITVSNFGAISGTFATPIVFDNQACIIGIGKMEKKLLLK
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Lipoamide acyltransferase, len: 449 as; Similarity to
Lipoamide acyltransferases. C. elegans lipoamide
acyltransferase (WP:ZK669.4) BLAST Score: 582, sum P(1)
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/note="predicted using hexExon; MAL3P2.2 (PFC0165w),
Hypothetical protein, len: 1676 aa"
/codon_start=1
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                                                                                                                                                                /protein_id="CAB38989.1"
/db_xref="G1:4493880"
/db_xref="SPTREMBL:097225"
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/note="predicted using hexExon; MAL3P2.4 (PFC0175w),
Hypothetical protein, len: 594 aa; Similarity with a
number of hypothetical proteins from model organisms.
C.elegans hypothetical protein (TR:001963) BLAST Score:
361, sum P(1) = 4.0e-47, 35% idenitity in 227 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                        DLKKCPNKPCPY I I OSVMLNNNV I CKCGY HFCFECLHEFHRPLLCSY I KKWY ELENN
DDHNMKWI HAYTKMCPNCNK P I EKNSCCMNVKC I CGY SFCWLCLDNWKNHKGGFYKCN
KY LEHNSKY NEQKKOK KKTDKKKDDTVKTY DDEKEDTDKTHDNDNI QNNREEKRNSHL
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RNNEFLKSANPIISPFSPGNIRNLENYYNNLIIQNLDQQNKQSNYYEHMNNQINYDNY
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/translation="mvKcNDSNQSkNCTRNFCNVNEEDRKEEGMMSQKDNENMYNPND
                                                                                                                                                                                                                                                                          /translation="mnipkeonkndoinvijeygkdkkkviktpindtkknniinhn
YDYSNINDKYNNTSDCYLMNNEDGINLYLNYYKKMFLKFOENNLYNYELKDIEKKME
LAILEIMNLINIQYDYAYHPLKAYNFNSNDLLENWFNNSKKVLTKLKLSHLKEEDILN
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GRNVERGYIEHPNLNIRNGARLIMNGPPVVQQEGIIIEHPTTEMHTSITSSGTREN
CFCNKNVQGNRQTNCYSLSGSCMCNPRIMGELKEKTNTMLHNPRIEQVFKPKIVKN
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HHNNNNIPSNVNFKSFHDNVITHNKINNMPYENNTVLKNNYSVNIPQTYTTKEFANN
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KILKWSYTYAYFSNWKSDNOKHLFEYHOGELEKNLDILQTKTEDINLTOFKNNTDNDT
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/note="predicted using hexExon; MAL3P2.7 (PFC0190c), PAST
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Hypothetical protein, len: 526 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"predicted using hexExon; MAL3P2.5 (PFC0180c),
Hypothetical protein, len: 895 aa"
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                                                                                                                                                                                /protein_id="CAB38990.1"
/db_xref="GI:4493881"
/db_xref="SPTREMBL:097226"
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db_xref="GI:4493883"
db_xref="SPTREMBL:097228"
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/gene="PFC0180c"
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/qene="PFC0185w"
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Db 136924 TAAATATATATATATATATATATATCCCCATTTTTGATGCTTTATTCATTATTCAATTT 136865
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                                                                        ttttacatttaaattagaatttttttttatcaataaatattaatttattagttttattaga 174
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 Length 153098;
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                                      Indels
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                                    508;
   DB 33;
 Score 91.2; DB 3 Pred. No. 0.0011;
                                    0; Mismatches
5.8%;
                                      Conservative
                     Similarity
                                      Matches 432;
     Query Match
Best Local 3
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18-APR-1994

PLN

DNA

5371 bp

YSCMTTGSA

gene

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DEFINITION
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                        Tzagoloff, A., Nobrega, M., Akai, A. and Macino, G. Assembly of the mitochondrial membrane system. Organization of yeast mitochondrial DNA in the Oill region (Lur. Genet. 2, 149-157 (1980) (2) notes that even though there are other possible coding sequences in the ds401 segment, none are sufficiently long to code for a gene product of the size of the varl protein. a model for the mitochondrial RNA processing is proposed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MOLVLAAKYIGAGISTIGLLGAGIGIAIVFAALINGVSRNPSIK
DTVFPMAIFGFALSEATGLFCLMVSFLLLFGV"
                                                                                                                                                                                                                       Assembly of the mitochondrial membrane system: The DNA sequence of a mitochondrial ATPase gene in Saccharomyces cerevisiae
J. Blol. Chem. 254, 4617-4623 (1979)
                                                         J01462.1 GI:343938
ATPase; proteolipid; transfer RNA; transfer RNA-Ser.
Yeast (S.cerevisiae) mitochondrial DNA; cytoplasmic petite mutants
(S.cerevisiae) mitochondrial Ser-tRNA and ATPase proteolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4287 TIATCTATATCATTTAAACTAATATATTTACTAAAAATATCACTATTAAATAAATATAT 4228
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Pred. No. 0.0032;
0; Mismatches 550; Indels
                                                                                                                   (rho-) ds400/a3 [1], ds401 [2].
Mitochondrion Saccharomyces cerevisiae
Eukaryota; Fungl; Ascomycota; Saccharomycetales;
Saccharomycetacee; Saccharomyces.
1 (bases 1026 to 2806)
Macino, G. and Tzagoloff, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Saccharomyces cerevisiae"
/organelle="mitochondrion"
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/product="tRNA-Ser"
/db_xref="SGD:S0007274"
352 c 368 g 72191 t
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ilarity 45.7%;
Conservative C
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Direct Submission Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK

1 (bases 1 to 67970) Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quall, M. and Barrell, B.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

malaria parasite P. falciparum Plasmodium falciparum

ORGANISM

AUTHORS

15-DEC-1999

PFMALIP3 67970 bp DNA INV Plasmodium falciparum MALIP3, complete sequence AL031746 GI:6594243

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LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
CSLKSLENINAVKKIPLNLLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
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AMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSQTDLFR
KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIOS
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NNNVDKIIITCTCLAEIDKSLKICETYDPEGKFLYLSAGVHPTNCYEFIDKNKHEEKE
On Dec 16, 1999 this sequence version replaced gi:5763807. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : I A K K E Y E E F I K Y F K N E Q V E N S K M E N G N K K I C D G E K D M N L N E I L L E K N L D T I P G F K Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aa, similarity: UPF0006 family eq to
YBL055C/YBL0512/YBL0511, YBF5_YEAST (418 aa), fasta
scores: opt: 316, E(): 1.1e-12, (33.2% identity in 271 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein, UPF0006 family"
/protein_id="CAB63556.1"
/db_xref="GI:6594244"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(1748. .2598,2748. .2848,2990. .3276))
/gene="MALLP3.01"
/note="MALLP3.01, conserved hypothetical protein, len
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contains possible signal sequence"
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complement(2742, .2747)
/gene="MALIP3.01"
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protein_id="CAB63557.1"
db_xref="GI:6594245"
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/protein_id="CAB63558.1"
/db_xref="G1:6594246"
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/gene="MALIP3.01"
/note="potential splice accomplement(2984. 2989)
/gene="MALIP3.01"
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/gene="MAL1P3.01"
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/gene="MAL1P3.01"
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/translation="MKKSYTFINVTILLFLTYYNYDTFSKTKFNNNIKIDIN RFKRIIAEASEEQKYPWEEDFCLILNEEELIRPEHNDSPYLPEHYENIDKINELSINS TKIWKETIKKMRONYEKETDNNNHNWRDFMWHYWANIYLYKHKLINITLKDLTNPI HDKETITTWIKWIQEDIEYFLFNLQVEWLRILTLELFYKNKE" COMPLEMENT (32477. 32486) YISFLKDFRVFSGLVVVMIMFPHLFFBALLHFYFHLFTINLKVSLMYFLYKINLCSNN HLQNRDAFYNTYRKFSSQTELDEISRDFLSICKNASSSSGTKNNKHNIDNNKFVEN DY IINFIKSTKKMENDSLNENSLPNVNIYNIMFSDVPSVTFFYTSCINLFNVFWIF MSFYVFHIKIGSNSVGIAIWLSIALYSAMILFEFLDSLFKSKYLIYRDKRIDNMHHVL GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRYLSLVRLYLN RHKYKIILIDEIPIFNLNNSVHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT /note="MALIP3.04, conserved hypothetical membrane protein, len: 203 aa, similarity: P. falciparum chromosome 2, PFB0110W, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity YLKDRLNKKEEIKFTSIIMPLYVYKILISNVANFPNLVNNVMEGIVNIKRLNNYINDH LYYNDIKNYFMYRTRYNEDYNIVVDKTFLQNENITSHDDGTSHNLKHLKNVIKNKLTN IILIYFFVFKRFSRGCKEAQRLYLSCHTPLCNIYSNALSGKNIINIYKKNTYHLDVYE LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL KITVEGRDIRTYNRKGEDSIIGILAQSSFVFYNWNIRTFIDPYNNFTDDEIVHALKLN /translation="MRIKMNSGIFFIKLLICISFICVFECFNKCMISYRKDLLMYSEN CFNYSIDRSLAEGSSESKETKVKDIPNIELLKSLNINYEEYEKMKEIVGSFMDNNNLN MFKYFFFYHKMNYHKNIINKQILSGLLKNVDDNTNKKICFQEHKSNSTYNYNSSHIHE KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINFN LKRNSLA I I IGNVGSGKSAFFHS I LGDFNMTHGNLY I ENFFKKMP I LYVPQNSWLFMG NIRSMILFGNEYNPLIYKYTILQSELLNDLSTIEHGDMKYINDDHNLSKGQKVRICLA RALYEHY I HMHKLCTDY EKKLIQPNEILDKDLI NNKNI SSYNNKKSKLVNYNI PFNEN YLQKCLMDDNNFYLYLLDDIFTSLDPSISKKIFSNLFCKEDNISFKDNCSFIISMNKS IDYTRIKLFDEVELNHVKHSNKMIYKEAYFVKGNTESVSFEIDSINKEYIKKMKKKNY KKEHMNKNNKDNNNNNNSNKDDHININMNDNHRNYNDINLGPNSTDDSPTVSSLGNE YTLDTYTSNNSDKEEIVKPLYKDTHEEFNKSSSMPFVKSSSNMINNPSNFKYEDNSSS FKGSISLETYLMYFQQVGFVLLTSVVIFMLISIFTDEIKFVFLTMMSIISKNNKEHSD TILQKQVRYLEYFVILDIISLVTSGICFSMIIYGNITSAIKVHNNILYSILNAPLYIF YNNNLGNIINRFIIDISAFDYGFLKRIYKAFFIFFRCILSSLLIIYMIRDCIFIFPFV NVITTOTYKEKNENISDKISAIVEYKNVSLSSIINSSQDDESKKKYGIKFENVYVSYK KKIPLVNGTYKY IDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISQG TLDNFLIEDILDNVQYEVNIFEIQDKTLKYRGNISEYMEKNNLNITKESHWGYSNLNT KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFF HYINNFRISYFFKWLINIWASLYIKIFILLLTTYIIMHPHLYASGIIKLYKEKNYVR) /noce-"region containing small subunit, 5.85 and large subunit rRNA genes and spacer regions" 23866. 31533 /gene-"rRNA aa. note="potential splice donor sequence, aaa/gtatat" /product="conserved hypothetical membrane protein, MAL1P3.04" join(36657. 36743,36864. 37343) /gene="MALIP3.05" /note="MALIP3.05, hypothetical protein, len: 188 /gene="MAL1P3.04" complement(join(31966. .32476,32675. .32775)) /gene="MAL1P3.04" /product="hypothetical protein, MaLIP3.05" /protein_id="CaB65560.1" /db_xref="G1:6594248" /note-"potential splice acceptor sequence" complement(32669, 32674)
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IANEVLKNIHSFTNI ENIFSLINDSSKSPVLKTFLKEFGSIFPHMLNNVPKLLFDLCQ
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                                                                                                                                                                              / John Paralpy 06, garp, len: 673 aa, similarity: identical to GARP_PLAFF (678 aa), fasta scores: 9 identity in 678 aa overlap."
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complement(40204. .40209)
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d="CAB63561.1"
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0; Mismatches 544;
              RNPLHIILGLIVILAAIYVFENFKNFEC"
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/gene="MAL1P3.05"
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 104992)
                                                     taatcggtaacattagactttcaaaatcatttttaacccctaaacagtaaatttgaagga
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* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary, Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
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Hyman,R.W., Oln,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
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                                                                                                                                                                                            Length 104992;
                    contig of $8642 bp in length
gap of unknown length
contig of 32169 bp in length
gap of unknown length
contig of 13781 bp in length.
                                                                                                                                              405 others
                                                                                                                                                                                                                     0; Mismatches 574; Indels
                                                                                                          /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/chromosome="12"
                                                                                                                                                                                             Score 89.6; DB 41;
Pred. No. 0.002;
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58842: 0
91011: 0
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73825 TITATTAATTAACTTAATTATATATATAAATAAATAAATTAATTGTGTAATTAAATTAA 73766
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 130281)
4 Whama, F.W., Fung, E.L., Qin, F., Rowley, D., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                     Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING PROGRESS ***, 3 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                863 actcacatc----caaacataacatggatatctccttaccaatcatactaattatttt
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 130281)
yman,R.W., Oln,F., Fung,E.L., Conway,A.B. and Davis,R.W.
irect Submission
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67462: gap of unknown length
82485: contig of 15023 bp in length
82685: gap of unknown length
130281: contig of 47596 bp in length.
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5.7%; Score 89.6; DB 60;
Best Local Similarity 47.3%; Pred. No. 0.0019;
Matches 534; Conservative 0; Mismatches 574;
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/db_xref="taxon:5833"
/chromosome="12"
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and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdqp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 133 contigs. The true order of the pleces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                RPCI-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA
ON Mar 8, 2000 this sequence version replaced 91:7025688
For further information about this sequence, including its location
                                                                                                                                                           AC008206 161891 bp DNA HTG 08-MAR-2000 Drosophila melanogaster chromosome 3 clone BACR03115 (D765) RPCI-96 03.1.15 map 968-968 strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blazej, R.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celniker, S.E., Agbayai, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.E., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                      Sukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Celliker, S. E., Agbayani, A., Arcaina, T. T., Baxter, E., Blazej, R. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C. M., Farfan, D. E., Galle, R., George, R. A., Harris, N. L., Hoskins, R. A., Harris, N. L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M. A., Mazda, P., Moshrefi, A., Moshrefi, A., Sequeira, A., Sethi, H., Shir, E., Seyleira, S. Sethi, H., Shir, E., Syirskas, R. R., Wan, K. H., Weinburg, T., Zhang, R., Zieran, L. L. a
                                                                                                                                                                                                                                                                                                                                                                                  terygota; Neoptera; Endopterygota; Diptera; Brachycera;
Auscomorpha; Ephydroidea; Drosophilidae; Drosophila.
[ (bases 1 to 161891)
                                          length
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of 740 bp in length
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Plasmodium falciparum MAL3P7, complete sequence. AL034559 AL008974 AL008985 AL008981 AL008983 AL009015 AL010138 AL010143 AL010146 AL010154 AL010155 AL010165 AL010187 AL010189 AL010207 AL010208 AL010214 AL021885 AL021888

253307 bp

PFMAL3P7

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PFMAL3P7 RESULT

LOCUS DEFINITION ACCESSION

11-FEB-2000

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Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and
Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                     The complete nucleotide sequence of chromosome 3 of Plasmodium
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Dasmodium falciparum
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
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NERBEKKKKLLDEDELMALNPEKSIKKOTISPIGHDEKSRHNEGMEEEEDDDEDD
DDEDDDDDSVDIKYRRKEKRSLLTKKYDKKEKHRRKSDHROKHRRENHSRHREK
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SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPFAFGLFKLQVYKNMKRYI
TSIYIXIYYYMLFVSCVIVDDLVNTDELIETIENLGLDNEQLQKKKQMDDDEENYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGLFDKIRNIEKLNEAELKNIGNNDSSWHDQYRDSSYIYIGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKDFLSYAENNDLNIFKLYNSEEDCLKNLKYAIELKSEDFKNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNNLLTPRYDEINELNKEREITMEYKKTDEK EYQVNNEY INENVGYDEKGGKYKTELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNDFFIYKMPMKSMKINAFDTFEKNIFRVVVFLCVCLFIVNICFDINKERKINIENFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCLK I NKYYYY Y SWLLFYFI I LFFYNI I FTLVVYFYVY KCLMNYFI LFFL I YFFLMNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLFTIICMOFSNNSSINYIATFLLFFLFSSFRLIIHSGASNILTFFVLLIPHSSFCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDFIFILIKNNIKIDYKQLFIKFENISLMHLIICSIVSFVLLICILNY I IYYKRKKMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M<u>L</u>NTKY RGKSKS ITNDKRKK SQQKTY EYGN I NYDMSEKYPTHQLKDNSNDFMLEGSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDTCYELDTLHKKQVNSQMCLRIEKIRNDRRESNGHPYDIPMIPLRHNNNINNNINNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIIQNVNKFYGKKHALKDVSLTLRSNRIFVLLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNDLEISYCSQNVILYENLTFYETIKIFLLYYNKNVDKYLNKKRTLKIMNDLDLVQYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICTHDIYEANNFANDIAVIKSGQIIFKGSKNSFQKLIEYKFTLNIQFNGLPNEEQTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNRDIIKKNIIKFIKGTRNENKNCFIFFNENHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTYKINELESLKKLLCVLNKFKNILTYQLKTIDIYYTYIYIYIYLNEKKKLLKNIQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLELNDDILNIHENDKNSLLYNLHTNIINLKSSEFNINDLYKDVYTENEFENIKNLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPH I LKVVKNTEFYKNF I KD I KNLKNENHYTQY FNDDRKKLFFY NFVKNNLVETKY SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLLSVENVNYYKKQKNVKFSYLFGLSPQSEGFKGKGLYKNAPLYNKYENKQYGNPFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYPYVTLESDKKINEKNERNEKNERNEKNERNEKNEKNGKNEKNKDILSSTNNNVYMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NG I QSYHNNNS I NSNDDQKKK NNNNNNY YYY NNPDGL I TNVKYK I RVGDYALLNSNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y FFNDININLKONFINFNTVDDLSFNIYFNEWYY FSFFIVLEY OFNSFILNY NADILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGSGKSTLINIITKMISKDSGEINFFKNSYKNKKKDIYMDVNKNRRNGLCGRICSNGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I KEFVANR I FK ROCNOT NYV DNNS NNNNNNNNNH SNNSC I NSSFNNNNNH NK EF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDQIKNLMDEVKKKISIFICFLVKRDIYILDEPFIALDIKTKTKLFKFFDKIKKNNII
                                                                                                                        /note="predicted using hexExon; MAL3P7.2 (PFCO865w),
RNA-binding protein, len: 310 aa; Similarity to C.elegans
RNA-binding protein. C.elegans RNA-binding protein
(TR:018318) BLAST Score: 378, sum P(1) = 3.8e-35; 37%
identity in 297 aa overlap."
                               join(5457. .5577,5689. .5787,5923. .6077,6189. .6743)
/gene="MAL3P7.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"predicted using hexexon, MAL3P7.3 (PFC0870w),
Elongation factor 1-beta, len: 181 aa; Similarity to
elongation factor 1-beta. A.salina elongation factor
1-beta (SW:EFIB_ARTSA) BLAST Score: 159, sum P(2) =
4.9e-16; 48% identity in 62 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using hexExon; MAL3P7.4 (PFC0875w),
iypothetical protein, len: 3004 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(7801. .7928,8084. .8306,8392. .8583)
/gene="MAL3P7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               فتر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref-"SPTREMBL:097318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB39068.1"
/db_xref="GI:4494009"
/db_xref="SPTREMBL:097319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB39024.1"
/db_xref="G1:4493965"
/db_xref="SPTREMBL:097278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNKNNSVDH I DHLFD I LVTN I NEFT
                                                                                                                                                                                                                                                                                                                                                                                       /protein_id-"CAB39067.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L NNN I NNN I NNN I NNN OH BNN OCK
                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="GI:4494008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDDEIGGLVQSAEIISFNKL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="MAL3P7.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene-"MAL3P7.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7801. .8583
/gene="MAL3P7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start-1
"MAL3P7
                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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VGVQRKKEQKKNRYTFFLKNFYLSNKEYKQPKENYEKNRNPFFYFIQKLFNLKRGNNV
DENNTTMGIYKYGEKVDSNNYISEDEININNQLNSEGYLKNDIYMNELNDNYNNDFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIIKNYTYCIHKLENKOKIKDSTILTKYPIDFFNKLLLKLYNIENNIYEIIKHEQLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITINNKSHNKVSËYLSSLFNILTLQINENHKOTLQLYKKLLDCEININILSREVQNIN
QITEMLNKKLDANIQKWKNIKNETTPP"
                                                                                                                      YLYYFIYILCLFIVLYIFDYKEFLFMSFFCFLLLYGFNIFLSICLFSSLYLHSYILFL
FFNFIFCGIISIVIYVLVILSYAYNNEILINLSHVLVCIFRIFDSFALSHVLNIRSLC
                                                                                                                                                                                     LNVKRHMKH I DED I MYEDMSNSNNFVI FGCFKKVY NQLSGDNNLN I SDG I QSVCEDSN
                                                                                                                                                                                                               SFFNTSGDFVFLLINCIIYLSIVFYKLLQIIPSKERTDKKNESEKTNYEEIILNNSYN
                                                                                                                                                                                                                                                                                                                                     KMRPYKIYTESSIFNNDLNILYFFKYFFCNNKDNLKGSLOTIAYGONYEINNKFINKK
NQNEHISEKIQKMNERDYKIELIPTMSIYEHFKIILTFKNIELTNVELKYIINLLMLI
                                                                                                                                                                                                                                                                                                                                                                                                  VNLKCDIHINÇNQLSGGMKKKVELMINLLRDDKIIFLYKLNDNIDFCSQIYINIILKN
                                                                                                                                                                                                                                                                                                                                                                                                                        ILLYNCEEDEHKDEYKDVYKDKYKDEYKDEYKDKYKDEYKDEYKOTYKOYEGYKYYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DILYYDYLYLFNKNKITYKNŸTTNIKNNFKKFYSFQIKLKGIRDSKIIDYVHMFFSIN
KHAFARFEKVIKKMDDKNSKKPKKKKKLISPKDMPSNSIILFLENNVKRNVLNVHNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSLQINKLTNIHFLNLLYFKYQNINTKYLFIHNKLYKYQDLLKSPLCFNDKENISSIF
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                                                                                      FHEHFMRDFYINIYVFLSIVIFFCVFFERFKNEIENRKIFENFHVHQYIHYFQILLLE
                                                                                                                                                                                                                                                                                                     NTVDIEMQISEKSNIKEKMLYKETEIDKYYKGQSDDDNDEEKNFNKISQKYILKNLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYIFKTMKKKKYNSKKKKGNLISLCKFHKILLNLMIDKYSYLHSYLSRNKYISIFHLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYWNNQKYYKYVNNFIYISPQKKRIMKNNKNLNNYNTIYDILLKYNMHSFTQDDTLC
ETLETRNDTDVNKEVEININLFYNYTSIHSYAYYTNSLFNMLSDFONILNKKSGNKNI
                               I LDGSTYDNI KVVEDVKGNCDMNTLLYDKENKYNYL I KDI DNKN I REECNANFRLSKN
                                                         VSYNNNEEEEDINGNINYNDSNNIYITPKKNNKEEENNFLVKKLKKRIDTLNEPFNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVYEQDIQLYKGEGIYTNDENQFDDYIDKYSLYDLRGKEDRKQLRENMLKGRHGKNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFDESNDISYTSNDVLKGDDDMLSLRRNTKESKRNKNKINKKKKKKENELILETYDIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNMNQLGSNLSNSNYLECNISSNMNSVNEPIIHSFIKENILKIKFGIENFVIYTHIY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFAICEVAYQNIQKFIIKYKGIKKVYSEITSMNNYVFILKIYDNKHIFKILGKQKKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MNIEERKKDIQTGIYEQEIFEELGQVLKEKFFKYINEANYEYYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEEKEDKNLINYNKYDKEFVCKDRKKNNTFITYDHIYSFMSFKKFSGKNISIDYNGS\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYHNFDINEVDNDIEEKIIKNTYRKKNLFNEHNYNKNIFYDNTKGQIILRIQNIKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD 119319 AAATAATTATATATATAAAAATATAATAATAGTATAAATTATAAATTGTACATATTA 119378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 ttattaattataattaaactgaaaacaatttggtatcaattcatatacatgcttagtaat 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aaaatgcgataattaattgataaatctgcaaaagattttacaaaatatctttcagaaaaaa 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"predicted using hexExon; MAL3P7.5 (PFC0880c),
Hypothetical protein, len: 478 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="predicted using hexExon; MAL3P7.6 (PFC0885c),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgctattcatcattttctaaccaaaccaatcttatatgttcttcaaattagaacttgaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 tagtittattagaaatattaattagaaaattitgaatooogattiotootootti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 253307;
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Pred. No. 0.002;
); Mismatches 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPIREMBL:097280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement(20964. .22397)
/gene="MAL3P7.5"
complement(20964. .22397)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(23721. .24665)
/gene="MAL3P7.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAB39026.1"
/db_xref="GI:4493967"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(23721. .24665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MAL3P7.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MAL3P7.6"
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release of this data is based on the understanding that the

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119439 AACGTTTACATTTATATATGTATTTATTTTTATAAGGATATACTTATATTT--ATATTA 119496
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PFMAL13PA 80518 bp DNA HTG 19-AUG-1999
Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN
                                                                                                                                                                                                                                                                           Harris, D., Lawson, D., Quail, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                 On Aug 24, 1999 this sequence version replaced gi:5731892. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: Th sequence is unfinished and does not necessarily represent the
                                                                                                                                                            malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct sequence. Work on the sequence is in progress and
                                                                                                                                                                                                                                                                        ., Churcher, C., Harris, B.,
                                                          PROGRESS ***, in unordered pieces.
                                                                                                            AL109815.2 GI:5763806
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                                                                                                                                           HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                 Barrell, B.
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SOURCE

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS TITLE JOURNAL

COMMENT

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sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector
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* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will

* be preserved.
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/strain-"3D7"
/db_xref-"taxon:5833"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkely Drosophila Genome Project (BDCP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the lisogenic strain y2; on bw sp, the same strain used for the BDGP's in the BDGP was a seminated by the BDGP from the board of the BDGP was a strain used for the BDGP's and a seminated by the BDGP from the board of the BDGP was a strain was a seminated by the BDGP was a seminated by th

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Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Droscophilidae; Droscophila.
1 (bases 1 to 843)
Genoscope.

Direct Submission

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

fly), genomic survey sequence. AL059666

AL059666.1 GI:4947129

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, filters for hybridization from the BACPAC Resource Center ca found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Location/Qualifiers

/organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCI-98"

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/clone="BACR26H19"

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CNSOOCS1 843 bp DNA GSS 04.JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR26H19 of RPCI-98 library from Drosophila melanogaster (fruit

RESULT 1 CNSOOCS1/c LOCUS DEFINITION

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AUTHORS REFERENCE

ACCESSION VERSION KEYWORDS SOURCE

DEFINITION

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Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the European Drosophila Genome Project (EDGP) -

http://www.edgp.ebl.ac.uk - This Drosophila melanogaster BAC

library (Dros BAC) was made by Alain Billaud at CEPH (Centre

d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton

pBeloBACII.
                                                                                                                                                                                                                        Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 caaactcacatccaaacataacatggatatctccttaccaatcatactaattatttggg
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 81.2; DB 123;
; Pred. No. 5.2e-05;
46; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila m
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_11b="DrosBAC"
/clone="BACN15C13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fly), genomic survey sequence. ALI03735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Drosophila melanogaster
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    GI:5622848
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Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL103735.1
  AL106627.1
                                                                       Drosophila
                                                                                            Eukaryota;
                                                fruit fly
                                                                                                                                                                                      Genoscope
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                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Collaboration of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Biland at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence SP6 end of BAC BACN15C13 of DrosBAC library from Drosophila melanogaster (fruit
      e survey sequence T7 end of BAC from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1085 АМҮММҮҮТТМАҮММТҮСТМТМАМТАМАААММАААММААММААММАТТТАҮАТТТНЫ 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1025 TAATHTAWIWYWCAATAHWWAWWITTATATWAATHTATTWATAHWTATYWTWHWATWY 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 agtggtgtgggagtaggcaacctggcattgaaacgagaaaagagagtcagaaccagaag 367
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                                                                                                                                     fruit fly.

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Neotera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilldae; Drqsophila.

1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 aagcattcatcatttaatacattaaaaaaatatttaatactaacagtagaatcttcttgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 tttaatttettaaaaaatgttgeaagacaettattagaeatagtettgttetgtttaeaa
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    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Drosophila melanogaster"
/plasmid-"pBeloBAC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 123;
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Pred. No. 2.8e-05
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BACNI6D22 of DrosBAC library fr
fly), genomic survey sequence.
AL106896
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/clone="BACN16D22"
/note="end : T7"
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Best Local Similarity 33.69
Matches 113; Conservative
                                                                                                                                                                                                                                                                                             rect Submission
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CNS016E1/c

RESULT

ACCESSION

Gaps

5

Indels

Length 1201;

others

120

us-09-464-528-16.rst

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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefêgenoscope.cns.fr
                                                                                                                                                            Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1197 ATTWAWTTATWTATWTATWTATWWTAATWWAWNTATAAATATAAATWTWWAWWAAAAWA 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 attttgataataaatatattttttttaatttcttaaaaaaatgttgcaagacact---tat 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tagacatagtettgttetgtttacaaaagcatteateattaatacattaaaaaaatatt 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila
1 (bases 1 to 1200)
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.1%; Score 79.8; DB 123; Length.
42.8%; Pred. No. 9e-05;
ive 57; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187
                                                                                                                                                                                                                                                                                                                                                                                               melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila mu
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="brosBAC"
/clone="BACN15E04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 42.8
Matches 115; Conservative
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                                                                                                            Direct Submission
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CNS00DKY/c
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DEFINITION
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                                                                                    AUTHORS
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                                                                   REFERENCE
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) + http://www.edgp.ebi.ac.ur. This Drosophila Welanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etudé du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1043)
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41.2%; Pred. No. 5.7e-05;
tive 58; Mismatches 158;
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/plasmid-"pBeloBAC11"
/db.xref-"taxon:7227"
/clone_lib-"brosBAC"
/clone="BACNIIG11"
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Best Local Similarity
Matches 153; Conserv
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             Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same straß, used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library of filters for hybridization from the BACPAC Resource Center can be
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Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 928;
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                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:727"
/clone_lib="RPCI-98"
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- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is anamed RPCI-99 and was constructed by partial Ecost disestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and the strain y2; cn bw sp, the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library and how to order individual BACR clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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BACROSN11 of RPCI-98 library from Drosophila melanogaster (fruit
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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41.1%; Pred. No. 0.00021;
tive 51; Mismatches 115;
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nes 116; Conserv
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COMMENT

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Per 19 91000 EVARI CHEARANTE (E-MMAIL): SequenceDectors.

Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on by sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACRAC Resource Center can be Location/Quallifiers
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSODYWL 1101 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACNO1G13 of DrosBAC library from Drosophila melanogaster (fruit
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroldea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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AL096927
AL096927.1 GI:5608538
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Matches 161; Conservative
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SOURCE
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                  Determination of this BAC-ded sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw 3p, the same strain was don't the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
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/clone_lib="RPCI-98"
/clone="BACR05N11"
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Matches 148; Query Match

29

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BASE COUNT ORIGIN

FEATURES

164

Gaps

284 834 344

REFERENCE

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS REFERENCE

RESULT 9 CNSOOFYG/C LOCUS DEFINITION

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Direct Submission
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TITLE
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                                                                      - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from empryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Determination of this BAC-end sequence was carried out as part of a Collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
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                                   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence T7 end of BAC: BAC29993 of RPCI-98 library from Drosophila melanogaster (fruit 14), genomic survey sequence.
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/plasmid-"pBeloBAC11"
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/clone_lib="DrosBAC"
/clone="BACN01G13"
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melanogaster genome using these BACS. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazucoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDCP from the isogenic strain y2; cn bw sp, the same strain used for the BDCP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library confilters for hybridization from the BACPAC Resource Center can be location/Qualiflers
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29B23"
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                                  Web: www.genoscope.cns.tr)
Determination of this BAC-end sequence was carried out as part of collaboration of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR04A23 of RPCI-98 library from Drosophila melanogaster (fruit
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP prosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's Pl and bST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library.

Gilters for hybridization from the BACPAC Resource Center can be contain at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
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                                                                                                  Submitted (02-UUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
                                                                                                                                                                            collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGM Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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- Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jons's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digastion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and by to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                 Compugen Ltd
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S-08-487-826B-13
S-08-731-722-3
S-08-731-722-3
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JS-08-449-043-36
JS-08-456-265A-36
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                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-446-855A-1
-08-565-907A-1
-08-910-551B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-107-755A-1
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                             243080 segs, 68777915 residues
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                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - nucleic search, using sw model
                                                                                                                                                                                                                               IDENTITY_NUC Gapoxt 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*
                                                                                                                                                                US-09-464-528-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4467
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                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                   Scoring table:
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                                                                    OM nucleic
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                                                                                                                                                                                                  Sequence:
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                                                                                                   Run on:,
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APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin zhaun
APPLICANT: Wellems, Thounas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                      Appl
Appl
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
COUNTRY: US
US-08-455-416-36
US-08-454-36
US-08-457-364-36
US-08-457-364-36
US-08-456-262-36
US-08-456-240-36
US-08-455-36-36
US-08-971-217-36
US-08-245-809-3
US-08-107-748-2
US-08-107-748-4
US-08-107-748-4
US-08-107-748-4
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ATTORNEY/AGENT INFORMATION:
NAME: STREASLEN, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  US-08-764-100-9
                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08487826B
Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                     2993
2993
3000
                                             12124
12124
12124
12124
12124
10395
10396
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10965
10965
642
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us-09-464-528-16.rni

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109 aagattttttaaaaaaatgtataaaattatatteattcatgattttcatacatttgattt 168
                                                                                                                                                                                                                                         169 tgataataaatatattttttttaatttcttaaaaaaatgttgcaagacacttattagacat 228
                                                                                                                                                                                                                                                                             479 TTATTAGAAGTATTTTCATTTTTAATTTTTTTAAAAGTTATATATCTTTAAAAAGATAT 420
                                                   Gaps
                                                                                                                         595 TATTGAAGAATTICTTATAACTACTATTAAAGATTTATAGGATCTACTGTATAAATCCAG
         Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 665
                                               Indels
Score 54.2; DB 4; L
Pred. No. 0.0089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                 0; Mismatches
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Pred. No. 0.
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27-JUN-1997
27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/08883795A Patent No. 5985607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Vectors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 40 King Street West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,20
         Query Match 7.5%;
Best Local Similarity 59.3%;
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             illarity 55.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (416) 364-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 361-1398 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                  229 agtcttgtt 237
                                                                                                                                                                                                                                                                                                                                                        419 AAATTAATT 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-883-795A-36
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                                                                                                                                                                                   1444 TTAGTATTTTAATAATAATAATCTTTTAAAAAACTTCAAAACATTTTTGCATAAAATA 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                    1504 ATATTAATATTAGTAACCACCTAGATAAATTAGAGAGAAAACGTAGAACATACCAAAAAA 1563
                                                                                     114 tttttaaaaaaatgtataaaattatattattcatgatttttcatacatttgattttgata 173
                                                                                                                                                                                                                                                                                                                    tgttctgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatactaacagt 293
                                                                                                                                                                                                                                                                                                                                                                                                294 agaatcttcttgtgagtggtgtgggagtaggcaacctggcattgaaacgagaaagaga 353
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Blocontrol of Fungal Soilborne Pathogens TITLE OF INVENTION: by Pythium oligandrum
                                                   0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1564 ATTAGAACAAAAGAATATTACAAAAATAATAAAATTAAATTA 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
           Score 56; DB 4;
Pred. No. 0.0053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Saliwanchik & Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08731722 Patent No. 5961971 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FELECOMMUNICATION INFORMATION
         Query Match
Best Local Similarity 47.7%;
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 32606-6669
OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin, Frank N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDIVIDUAL ISOLATE: 23-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEO ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1186 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LASSIFICATION:
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US-08-731-722-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-731-722-5
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620 Newport Center Drive
                                                                                                                                                                                                                                                   Sequence 13, Application US/08487826B
                                                                                                                                                                                                                                                                                                                                                                              Su, Xin-zhaun
Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                           Peterson, David S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (619) 235-8550
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LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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Best Local Similarity 53.0'
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Israelsen, Ned
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newport Beach
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                         Patent No.
                  657
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                                                                                                                            taatttottaaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaa 249
                                                                                                                                                             108 aaagattttttaaaaaaatgtataaaattatattattcatgattttcatacattgatt 167
                                                       85 TATAATTAAAATATTATAATTAA--ATATTTAATTAAAATATTTAAATTAAATAT 142
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   ö
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APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8920;
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                                                                                                                                                                                         geatteateataeattaaaaaaaatatttaataetaaeagta 1294
                                                                                                                                                                                                                       S: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 3;
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/446,855A FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.2
                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08446855A Patent No. 5849573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.00
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT' INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: genomic US-08-446-855A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING TEMP PC-DOS/MS-DOS
SOFFMARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
                                                                                                                         537 AATTATAGGAACCACAATATTGGGGAGT 510
                                                                                   288 aacagtagaatcttcttgtgagtggtgt 315
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230 gtcttgttctgtttacaaaagcattcatcatttaatacattaaaaaaatat 279
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                                      15789 ATATTTTTTTTTAACATTTTTTAAT-TTTTTTTTTATTTTATGATATATTTTTATTT 15731
142 attoatgatttttcatacatttgattttgataataaatatatttttttaatttcttaaa 201
                                                                               202 aaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattcatcatt 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 agattttttaaaaaaatgtataaaaattatattattoatgatttttoataoatttgatttt 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 ATTTTCTGTTAAAAAATAAAACCTTTCTCTATTGAAGAATTTTTATAGCTACTGTTA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                               Blocontrol of Fungal Soilborne Pathogens
by Pythium oligandrum
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51.2; DB 4;
Pred. No. 0.038;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08731722
Patent No. 5961971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERNEC/COCKET NUMBER: UF-
TELECOMMUNICATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: 1986-41
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JOURNAL SOURCE:
TAINTAL SOURCE:
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Matches 125; Conservation
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Martin, Frank N.
TITLE OF INVENTION: Blocont.
TITLE OF INVENTION: by Pyth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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15730 TAATATAT 15722
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                                                                                                                                                                                                                                                         RESULT 6
US-08-731-722-3
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3429 ATTATTTATTCTTATTAAAATATTATGATTATTAATAAAGTAGAATAAGG--ATTACA 3372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                           TITLE OF INVENTION: Biocontrol of Fungal Soilborne Pathogens TITLE OF INVENTION: by Pythium oligandrum NIMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3251 GTAGAATTGAGAGAATAAATACTTCTAATTTACTTTATATAATAT 3202
683 GTAGAATTGAGAGAAATAATACTTCTAATTTACTTTATTAATAT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 gtcttgttctgtttacaaaagcattcatcatttaatacattaaaaaatat 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51.2; DB 4; Length 3 Pred. No. 0.038; 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                              ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/731,722
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; Sequence 36, Application US/08883795A
                                                                                                            Sequence 3, Application US/08731722
Patent No. 5961971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: .linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 7.1%;
Best Local Similarity 54.3%;
Matches 125; Conservative
                                                                                                                                                                                          Frank N.
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3933 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Whitlock, Ted W. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single.
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                             Gainesville
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Martin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                        JS-08-731-722-3/c
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Martinus

us-09-464-528-16.rni

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448 TATAAAATATGTAATTATAAAGATTTTAATTATAAAATATGTAATTATAAAGATTTTAAT 389
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                                   DNA Molecules and Expression
                                                     Tissue Plasminogen Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 4; Length 665;
Pred. No. 0.035;
0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                           URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08764100 Patent No. 5773700
                               Recombinant
Vectors for
Genevieve
                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                    ADDRESSEE: BERESKIN & PARR STREET: 40 King Street West CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.18;
ilarity 53.08;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Rh 32
                 Gregor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
           APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recc
TITLE OF INVENTION: Vect
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN 6
                                                                                                                                                                                   COUNTRY: Canada
21P: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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Best Local Similarity
Matches 131; Conserv
                                                                                                                                                               STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                 COUNTRY:
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187 ttttaatttettaaaaaatgttgeaagacaettattagacatagtettgttetgtttaca 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 473,
                         TITLE OF INVENTION: Improvements in or Relating to Organic TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                               UPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 103;
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Pred. No. 0.047;
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                                                                               E: Sandoz Agro, Inc
975 California Avenue
               Goldbach, Robert W.
                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.0%;
Best Local Similarity 52.1%;
Matches 112; Conservative
  Peters, Dirk
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                              OMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                          Palo Alto
                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                94304
                                                                                ADDRESSEE:
APPLICANT:
APPLICANT:
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an Grinsven J., Martinus Q

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1293 TTTTTATTGTTTTATACATTTTATTGTTTTTGTTGATTTTTATTTTATTATTTTTA 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 ttttaatttcttaaaaaatgttgcaagacacttattagacatagtcttgttctgtttaca 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4970;
                                                                                                       TITLE OF INVENTION: Improvements in or Relating to Organic TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50.2; DB 2;
Pred. No. 0.06;
0; Mismatches 103;
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van Grinsven J., Martinus Q.
De Haan, Petrus T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/214,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: NO. 5773700ris, Allen E. REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/032,235
ELITING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
                                           Johannes J
                                                                                                                                                                                            ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
                                                                                       Goldbach, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 14:
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52.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4970 base pairs
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                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                           ielen L.,
                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 112; Conserva
                                                                                                                                                                                                                                          Palo Alto
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                                                                                                                                                                                                                                                                                                          94304
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                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                     APPLICANT:
                                                              APPLICANT
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3678 TITITATITICITITATACATITICITITICITICATITITATITITATITITA 3619
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                                                        TITLE OF INVENTION: Improvements in or Relating to Organic TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 103; Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DALE.
APPLICATION NUMBER: very PILING DATE: 19-WAR-1992
FILING DATE: 19-WAR-1992
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT NIVORMATION: 34,490
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/764,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/214,064
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Gielen L., Johannes J
                                                                                                                                     ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
CITY: Palo Alto
                                    Goldbach, Robert W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.08;
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N: 800
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(415) 857-1102
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FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 93
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nucleic acid
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Best Local Similarity 52.1°
Matches 112; Conservative
                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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RESULT 11 US-08-764-100-20/c ; Sequence 20, Application US/08764100 ; Patent No. 5773700

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FRAGMENT TYPE: ORIGINAL SOURCE:
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                                                                                                                                                                                                     USA
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                                                                                                                                                             Okemos
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 attigattttgataataaatatattttttttaatttcttaaaaaaatgttgcaagacactt 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 at-tagacatagtettgttetgtttacaaaageatteateatttaataeattaaaaaata 278
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Pred. No. 0.064;
0; Mismatches 123; Indels 1
                                                 APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
                                                                                                                                          E: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sylvain Moineau, Barbara
J. Holler, Peter A. Vandenbergh,
Ebenezer R. Vedamuthu, Jeffrey K
                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.24
:URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                        MEDIUM, TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08565907A Patent No. 5814499
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET UNMBER: 47
FELECOMMUNICATION:
TELEPHONE: 703-816-4000
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                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 06-JU1-1995
CLASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
NAME: MICCHARD, Leonard C
REGISTRATION NUMBER: 29.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.0%;
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Best Local Similarity 52.1
Matches 135; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                COUNTRY: USA
2IP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                     Virginia
                                                                                                                                                                                  Arlington
SENERAL INFORMATION: APPLICANT: Stewar
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US-08-565-907A-1/c
                                                                                                                                          ADDRESSEE:
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APPLICANT:
APPLICANT:
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Length 4467;
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pred. No. 0.071;
0; Mismatches' 132;
DNA Encoding Phage
Abortive Infection Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: N/A
IDENTIFICATION METHOD: sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: phage abortive infection
                                  From Lactococcus
                                                                                                                                                                                                                                                                                                                                    US/08/565,907A
                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS (version
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch,
MEDIUM TYPE: 360 KD storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance
                                                                                                                                                                                                                                                                                                                                                   December 1, 1995
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                                                                                                                  2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20,931
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                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect.5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE...
HAPLOTYPE.
TISSUE TYPE: N/A
FELL TYPE: bacterium
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Best Local Similarity 49.4
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: NO. 5814499e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single
                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE:
              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDIVIDUAL ISOLATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
                                                                                                                                                           STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                  Acer
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Gaps

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Indels

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2679 ATTTAAATCAATTAAGTTTAGTAATTCTTCTTGATTTAATAAATCATCTATTTCAAAGAC 2620
                                                                                                                            2619 AACCATATACAACAATATTIGATATAATTCTTGATAAAATTATTTTTACGATAGTGGTC 2560
                                                                                                                                                                                                          2559 TATITITICITITAAGCCCTITGAATTATTACTAAATATITITTACAATATTITGAAGC 2500
                                                                                                                                                                                                                                                       228 tagtottgttotgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatact 287
aaagattttttaaaaaaaatgtataaaattattattcatgattttcatacatttgatt 167
                                                                                                                                                                       168 ttgataataaatatatttttttaatttcttaaaaaatgttgcaagacacttattagaca 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             From Lactococcus
lactis, and Method of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Encoding Phage
Abortive Infection Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sylvain Moineau, Barbara
J. Holler, Peter A. Vandenbergh,
Ebenezer R. Vedamuthu, Jeffréy K
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August 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS (version SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch.
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08910551B Patent No. 5910571
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ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Ian C. McLeod
2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                  2439 TAATCTTGAATCTTTAATGA 2419
                                                                                                                                                                                                                                                                                                                                          288 aacagtagaatcttcttgtga 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Nucleotide
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ian C. McLeod
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michigan
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-08-910-551B-1/c
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2559 TATTITITICITITAAGCCCTTTGAATTATTACTAAAATATTITITACAATATTTGAAGC 2500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 ttgataataaatatatttttttttaatttcttaaaaaaatgttgcaagacacttattagaca 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 4467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.9%; Score 49.8; DB 4;
19.4%; Pred. No. 0.071;
Lve 0; Mismatches 132;
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From Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sylvain Moineau, Barbara
J. Holler, Peter A. Vandenbergh
Ebenezer R. Vedamuthu, Jeffrey
                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD: sequencing OTHER INFORMATION: DNA encoding phage OTHER INFORMATION: resistance
                                                                                                                                                                                                                                                                                  phage abortive infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08909425A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2439 TAATCTTGAATCTTTAATGA 2419
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                                   Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 aacagtagaatcttcttgtga 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.9%;
Best Local Similarity 49.4%;
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                      , PUBLICATION INFORMATION:
US-08-910-551B-1
                                                                                                                                                                                                                                                                                                    LOCATION: N/A
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. MC
                                                                                                                                         bacteriur
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                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                              LIBRARY: genomic
CLONE: SMQ-20
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Michigan
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                                                                                                          Z/A
                                                                                                                                                                                           MMEDIATE SOURCE:
                  SOURCE:
                                                                                                         HAPLOTYPE: N
TISSUE TYPE:
FRAGMENT TYPE:
ORIGINAL SOURCE
                                                                                                                                       CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-909-425A-1/c
                                 ORGANISM:
                                                                                                                                                                                                                                                                                   NAME/KEY:
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APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 5.25 inch,

COUNTRY:

Search completed: September 2, 2000, 02:01:16 Job time: 8440 sec

288 aacagtagaatcttcttgtga 308 | | | | | | | | | | | | 2439 TAATCTTGAATCTTTTAATGA 2419

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us-09-464-528-16.rni

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MEDIUM TYPE: 360 Kb storage
COMPUTER: Acer
OPERATING SYETEM: MS-DOS (version 4)
SOFWARE: Wordperfect 5.1
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,425A
FILING DATE: MOUST 11, 1997
CLASSIFICATION NUMBER: US/08/909,425A
FILING DATE: December 1, 1995
ATTORNEY ARENT INFORMATION:
NAME: Ian C. McLeod
TELECOMMUNICATION INFORMATION:
NAMI: SENSE: NA/A
ORGANISM: Lactococcus lactis
STRAIN:
INDIVIDUAL ISOLATE: W1
NAMI: SENSE: NA/A
TISSUE TYPE: NA/A
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2619 AACCATATACAACAATATTGATATAATTCTTGATTAAAATTTTTTACGATAGTGGTC 2560
                                                                                                                                                                                                                                                        2559 TATTITITITAGCCCTITGAATTATTACTAAATATTITITACAATATTITGAAGC 2500
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Query Match 6.9%; Score 49.8; DB 4; Length 4467;
Best Local Similarity 49.4%; Pred. No. 0.071;
Matches 129; Conservative 0; Mismatches 132; Indels 0; Gaps
                                                                                  108 aaagattttttaaaaaaatgtataaaaattatattcatgattttcatacatttgatt 167
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ברת:		<pre>September 2, 2000, 02:07:29 ; Search time 161.21 Seconds (without alignments) 1115.862 Million cell updates/sec</pre>	3	1 agatcaaactcacatccaaagtttttgaagtataaagatg 719
	mode1	2:07:2		p1
copi ranc (c) 1333 compagai pro:	arch, using sw	ber 2, 2000,- 0	US-09-464-528-16 719	caaactcacatccaa
T L L	cleic sea	Septem	US-09-	1 agat
	OM nucleic - nucleic search, using sw model	Run on:	Title: Perfect score:	Sequence:

311585 seqs, 125096042 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Scoring table:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cDNA encoding Plas	Plasmodium berghei	Sequence encoding	Plasmodium var-7.g	Pythium oligandrum	Borrelia burgdorfe	Human 3' apolipopr	bur	Orpinomyces cellul	Orpinomyces cellul	pNPX30 xylanase cD	Carbamoy1-phosphat	Human 3' apolipopr	Malaria-specific g	SERP gene. Recombi	Sequence encoding	Borrella burgdorfe	cDNA encoding Plas	Plasmodium var-7 g	Borrelia burgdorfe	Plasmodium berghet	Sequence of ANS-1	Pythium oligandrum	Pythium oligandrum	MS-Le1610 Vector.	ontinuation	P.falciparum GBP13	Impatiens Necrotic	Sequence encoding	Carbamoyl-phosphat	Sequence encoding	pSRQ800 fragment 1	Thymidylate phosph
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ID	T41852	V33135	N60472	T72882	V29580	X20251	T31530	X20253	V37413	V29477	053480	062924	T31530	N81157	022999	003568	X20253	T41852	T72882	X20361	V33136	N71405	V29578	V29578	055185	V21209	027886	049959	003568	062924	025273	T68648	012528
DB	-	Н	-	-	-	Ħ		-	-	-4	-	-	Н	ч	-	-	-	-	-	-	-	-	-	Н	-	-	-	-	Ä	-	-	н,	-
Length	9789	5849	4590	19124	1186	53585	605	26811	1826	1826	2503	-8920	605	3975	3975	6124	26811	9789	19124	783	1711	1864	3933	3933	1470	110000	2418	4970	6124	8920	2104	4467	1611
Ouery Match	8.4	7.8	7.8	7.8	7.5	7.4	7.3	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.2	7.2	7.2	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0	7.0	7.0	6.0	9
Score	60.2	56.4	26	26	54.2	53.2	52.6		52.2	52.2	52.2	52	51.8	51.8	51.8	51.8	51.8	51.4	51.4	51.2	51.2	51.2	51.2	-	51	50.8	50.2	50.2	50.2	0	20	49.8	4.6
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	Ouery Score Match Length DB ID	Ouery Score Match Length DB ID 60.2 8.4 9789 1 741852 CDNA encoding	Ouery Score Match Length DB ID 60.2 8.4 9789 1 T41852 56.4 7.8 5849 1 V33135	Ouery Score Match Length DB ID 60.2 8.4 9789 1 T41852 56.4 7.8 5849 1 V33135 56 7.8 4590 1 N60472	Ouery Score Match Length DB ID 60.2 8.4 9789 1 T41852 56.4 7.8 5849 1 V33135 56 7.8 4599 1 N60472 56 7.8 19124 1 T72882	Ouery Score Match Length DB ID 60.2 8.4 9789 1 T41852 56.4 7.8 5849 1 V33135 56 7.8 4590 1 N60472 56 7.8 19124 1 T72882 54.2 7.5 1186 1 V29580	Score Match Length DB ID 60.2 8.4 9789 1 T41852 56.4 7.8 5849 1 V33135 56 7.8 4590 1 N60472 56 7.8 4590 1 N60472 56 7.8 19124 1 T72882 57 7.8 19124 1 V29580 54.2 7.5 5188 1 BOTCHIM OF S3.2 7.4 53585 1 X20251	Ouery Score Match Length DB ID Descripti 60.2 8.4 9789 1 741852 CDNA enco 56.4 7.8 5849 1 73135 Plasmodiu 56 7.8 19124 1 772882 Sequence 56 7.8 19124 1 772882 Plasmodiu 54.2 7.5 1186 1 V29580 Pythium of 53.2 7.4 45368 1 Authium of Bythium of 52.6 7.3 605 1 73536 Human 3 Human 3	Ouery Score Match Length DB ID Descripti 60.2 8.4 9789 1 T41852 CDNA enco 56.4 7.8 5849 1 V33135 Sequence 56 7.8 4590 1 N60472 Sequence 56 7.8 19124 1 T72882 Plasmodlu 54.2 7.5 1186 1 V29580 Pythium o 53.2 7.4 53585 1 X20251 Borrella 52.4 7.3 26811 1 X20253 Borrella 52.4 7.3 26811 1 X20253	Score Match Length DB ID 60.2 8.4 9789 1 T41852 CDNA enco 56.4 7.8 5849 1 V33135 Sequence 56 7.8 4590 1 N60472 Sequence 56 7.8 19124 1 T72882 Plasmodiu 54.2 7.5 1186 1 V29580 Plasmodiu 53.2 7.4 53585 1 X20251 Plasmodiu 52.6 7.3 665 1 T31530 Pummn 3' 52.4 7.3 1861 1 X20253 Borrella 52.2 7.3 1826 1 V37413 Orphinomyo	Ouery Score Match Length DB ID Descripti 60.2 8.4 9789 1 741852 CDNA enco-CDNA enco-	Ouery Score Match Length DB ID 60.2 8.4 9789 1 741852 CDNA encoconstruction 56.4 7.8 5849 1 933135 Plasmodiu 56.4 7.8 4590 1 M60472 Sequence 56.7 7.8 19124 1 772882 Plasmodiu 56.7 7.5 1186 1 V29580 Pythium o 53.2 7.5 1186 1 V29580 Pythium o 52.6 7.3 26811 1 X20251 Human 3' 52.4 7.3 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Sequence 56 7.8 19124 1 T72882 Plasmodlu 54.2 7.5 1186 1 V29580 Pythium o 53.2 7.3 186 1 V29580 Borrella 52.6 7.3 26811 1 X20253 Borrella 52.7 7.3 1826 1 V29477 Corpinomyc 52.2 7.3 1826 1 V29477 Corpinomyc 52.2 7.3 2503 1 G53480 PyR330 xy 52.2 7.3 2503 1 G53480 CORPINOMY 52.2 7.3 2503 1 G53480 CORPINOMY 52.2 7.3 2503 1 G53480 CORPINOMY 52.3 7.3 2503 1 G53480 CORPINOMY 52.3 7.3 2503 1 G53480 CORPINOMY 52.3 7.3 3503 1 G53480 CORPINOMY 52.3 7.3 8920 1 G62924 Human 3** 51.8 7.2 8920 1 G62924 Human 3** 51.8 7.2 8950 1 M81157 MALARIA**	Ouery Score Match Length DB ID Descripti 60.2 8.4 9789 1 T41852 CDNA enco- 56.4 7.8 5849 1 V33135 CDNA enco- 56.4 7.8 4590 1 NG0472 Sequence 56 7.8 19124 1 T72882 Plasmodlu 54.2 7.5 1186 1 V29580 Pythium o 53.2 7.4 53585 1 X20251 Pythium o 52.4 7.3 26811 1 X20253 Borrella 52.4 7.3 1826 1 V37413 Corpinomyo 52.2 7.3 1826 1 V29477 Corpinomyo 52.2 7.3 1826 1 V37413 Corpinomyo 52.2 7.3 1826 1 N31480 Carbamoyl 51.8 7.2 6920 1 G62924 Carbamoyl 51.8 7.2 6920 1 G22999 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1826 1 V37413 52.2 7.3 1826 1 V37413 52.2 7.3 1826 1 V37413 52.2 7.3 1826 1 V29477 52.2 7.3 1826 1 V29477 52.2 7.3 1831 1 M81157 51.8 7.2 605 1 T41852 51.4 7.1 19124 1 T72882 51.4 7.1 19124 1 T72882 51.2 7.1 783 1 X20361 51.2 7.1 1864 1 N71405	Ouery 60.2 Match Length DB ID 60.2 8.4 9789 1 T41852 56.4 7.8 5849 1 V33135 56.7 7.8 19124 1 T72882 54.2 7.8 19124 1 T72882 54.2 7.5 1186 1 V29580 52.4 7.3 1865 1 T31530 52.2 7.3 1826 1 V37413 52.2 7.3 1826 1 V3947 51.8 7.2 6029 1 G62924 51.8 7.2 26811 1 X20259 51.8 7.2 26811 1 X20259 51.4 7.1 9789 1 T41852 51.4 7.1 1978 1 T72882 51.2 7.1 1978 1 T72882 51.2 7.1 1711 1 V33136 51.2 7.1 1711 1 V33136	Ouery Score Match Length DB ID 60.2 8.4 9789 1 T41852 56.4 7.8 5849 1 V33135 56.4 7.8 5849 1 V33135 56.4 7.8 19124 1 V33135 54.2 7.8 19124 1 T72882 52.4 7.8 5885 1 X20251 52.6 7.3 26811 1 X20251 52.2 7.3 26811 1 X20251 52.2 7.3 26811 1 X20251 52.2 7.3 2503 1 Q53480 52.2 7.3 2503 1 Q53480 52.2 7.3 2503 1 Q53480 52.2 7.3 2503 1 Q53294 51.8 7.2 605 1 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7.8 19124 1 T72882 52.4 7.3 26811 1 X20251 52.2 7.3 1826 1 V29477 52.2 7.3 26811 1 X20251 52.2 7.3 1826 1 V29477 51.8 7.2 6124 1 Q65299 51.4 7.1 19124 1 T72882 51.2 7.1 19124 1 T72882 51.2 7.1 19124 1 V33136 51.2 7.1 19124 1 V33136 51.2 7.1 19124 1 V33136 51.2 7.1 1910 1 V31209_11 50.2 7.1 1000 1 V21209_11 50.2 7.0 4970 1 Q65186	Ouery Score Match Length DB ID 60.2 8.4 9789 1 T41852 56.4 7.8 5849 1 V33135 56.4 7.8 19124 1 V33135 56.7 7.8 19124 1 T72882 54.2 7.8 19124 1 T72882 52.2 7.3 26811 1 X20253 52.2 7.3 2503 1 Q53480 51.8 7.2 3975 1 Q03568 51.8 7.2 26811 1 X20299 51.8 7.2 26811 1 X20253 51.4 7.1 19124 1 T72882 51.2 7.1 19124 1 T72882 51.2 7.1 19124 1 T72882 51.2 7.1 110000 1 V21209 51.2 7.1 11470 1 Q55185 50.2 7.0 4318 1 Q23886	Ouery Score Match Length DB ID 60.2 8.4 9789 1 741852 56.4 7.8 5649 1 V33135 56.4 7.8 5649 1 V33135 56.4 7.8 19124 1 V33135 56.4 7.8 19124 1 T72882 55.2 7.8 19124 1 T72882 52.2 7.3 186 1 V29580 52.2 7.3 1826 1 V29580 52.2 7.3 1826 1 V294713 52.2 7.3 1826 1 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7.2 3975 1 081157 51.8 7.2 3975 1 772882 51.4 7.1 19728 1 772882 51.2 7.1 19728 1 772882 51.2 7.1 11000 1 V21209 50.2 7.0 6124 1 003568 50.2 7.0 6124 1 003568 50.2 7.0 6124 1 003568 50.2 7.0 6124 1 003568 50.2 7.0 6124 1 003568 50.2 7.0 6224 50.2 7.0 6224 50.2 7.0 6224 50.3 7.0 6224 50.3 7.0 6224

Borrelia burgdorfe Tox2a gene. DNA en	pNPX30 xylanase cD 50 kD subunit of S	Medium chain-speci P. falciparum live Continuation (13 o	P. falciparum live Continuation (14 o	Malaria-specific P Gmhsp26-A heat sho	Borrelia burgdorfe
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ALIGNMENTS

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24-AUG-1991
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                                                                                                                                                                                                                                                                                                                               293 tagaatcttcttgtgagtggtgtgggagtaggcaacctggcattgaaacgagagaaagag 352
                                                                Disclosure: Figure 12: 149pp; English.

A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte membrane protein (PfEMPI) or active fragments or analogues of that protein can be used in the treatment or prevention of symptoms of a malaria parasite infection. The polypeptides can inhibit, block or reverse the sequestration of erythrocytes in patien, suffering from malaria. Nucleic acids derived from the PfEMPI gene can be used as probes and primers to identify a Plasmodium falciparum parasite, the primers used to generate characteristic amplification patterns from different P. falciparum strains. Antibodies specifically immunoreactive with the PfEMPI polypeptide or its fragments may be used in diagnosis of malaria infection. This sequence encodes the pfEMPI protein of the MC type of Plasmodium falciparum. An
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                       truncated version of the coding sequence (a cDNA clone)
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0
                                   New Plasmodium falciparum erythrocyte membrane proteins - used. develop products for the diagnosis, treatment or prevention of malaria parasite infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2498 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60.2; DB 1; Length 9789;
Pred. No. 0.04;
0; Mismatches 183; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1998 (first entry)
Plasmodium berghei plastid PSI-PL470 gene.
Malaria; infection; therapy; diagnosis; vaccine; plastid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting Plasmodium infection from hybridisation with
                                                                                                                                                                                                                                              1837 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) INST MOLECULAR & CELL BIOLOGY.
(UYSI-) UNIV SINGAPORE NAT.
Kara AKU, Nelson JS, Tan TMC, Tham JM, Ting RCY;
WPI; 98-447251/38.
                                                                                                                                                                                                                                              1393 C;
  Pasloske BL;
                                                                                                                                                                                                                                              4061 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium berghei ANKA strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V33135 standard; DNA; 5849 BP.
                                                                                                                                                                                                                                                                                 8.4%;
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.21
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU-009481.
AU-004953.
AU-006329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-1998; IB0212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS1-PL470 gene; ds
                                                                                                                                                                                                                                  is given in T41853
                       P-PSDB; W00384
                                                                                                                                                                                                                         alternative,
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                                                                                                                                                                                                                                               Sequence
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This is the nucleotide sequence of one strand of the PSI-PL470
gene of the 30.7 kb extrachromosomal plastid of Plasmodium berghel.
This plastid encodes organelle-like rRNAS, tRNAS, trNAS, ribosomal
proteins and RNA polymerase subunits, amongst others. Plasmodium is
cletected in a human or animal sample by treating it, or derived
cucleic acid, with a Plasmodium extrachromosomal genetic element or
derived nucleic acid (A) and detecting any hybridisation. (A) can
include the PSI-PL470, PLH-PPH, PRB or PWO gene, the mitochondrial
cori gene, and nucleic acids derived from them. Also new are
include the PSI-PL470, PLH-PPH, PRB or PWO gene, the mitochondrial
cori gene, and nucleic acids derived from them.
Also new are
(A)-Specific probes and primers (see V33139-56). The method is
used to diagnose Plasmodium infection. Also (not claimed) the
cused to diagnose Plasmodium infection. Also (not claimed) the
cused to development of an anti-malaria vaccines. The high
development and for development of anti-malaria vaccines.
Cevelopment of genus- or species specific assays that result in
fewer false negatives than known methods (typically 1% against 3%).
Sequence 5849 BP; 2296 A; 673 C; 2323 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 ttttcatacatttgattttgataataatatttttttttaattcttaaaaaatgttgc 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 tattaattaagaaattaaaagattttttaaaaaaatgtataaaaattatatteateat 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614 ATGGATTAAATATATATTGATAAAAATTTATCTAATAATATTTTTTATATTTTTTTA 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 atatctccttaccaatcatactaattattttgggttaaatattaatcattattttaaga 90
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providing genus or species specific egatives, in humans or animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 7.8%; Score 56.4; .DB 1; Length 5849; Best Local Similarity 53.1%; Pred. No. 0.16; Matches 120; Conservative 0; Mismatches 106; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                האה כסטוחק וסר Plasmodium falciparum antigens - expressing
poly:peptide(s) having antigenicity of RESA or FIRA antigens
falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The inventors claim a novel DNA molecule which comprises a nucleotide sequence corresp. to all or a portion of the base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kemp DJ, Anders R, Coppel RL, Brown G, Saint RB, Cowman AF;
WPI: 86-094065/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 aagacacttattagacatagtcttgttctgtttacaaaagcattca 256
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                                       iagnosis with few false negatives, it
laim 15; Page 54-59; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malaria vaccine; antigen; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N60472 standard; DNA; 4590 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 1; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= a
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HALL-) HALL INST MED RES
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-SEP-1984; AU-007067
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us-09-464-528-16.rng

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Claim 4: Page 56-61; 96pp; English.

This sequence represents the var-7 gene of Plasmodium. Var-7 belongs to This sequence represents the var-7 genes which have homology to the Duffy binding like (DBL) family of genes which have homology to the Duffy antigen binding protein (DABP) and sialic acid binding protein (SABP) conserved regions (see T72889 and T72888 respectively). The var family of genes modulate cytoadherence and antigenic variation of Plasmodium infected erythrocytes. SABP and the Duffy antigen binding protein (DABP) are soluble proteins that appear in the culture supernatant after infected erythrocytes release merozoites. DABP and SABP mediate the binding of merozoites and schizonts to the erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmodium var-7 gene.

DBL gene family; SABP; stalic acid binding protein; vaccine; therapy;
Duffy binding like gene; Duffy antigen binding protein; erythrocyte;
DABP; merozoite; malaria; var-1; var-2; var-3; var-7; immune response;
                                                                                                                                                                                                                                                                                                                         49 tactaattattttgggttaaatattaatcattattttaagatattaagaaattaa 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgataataaatatattttttttaatttcttaaaaaatgttgcaagacacttattagacat 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 agtottgttctgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatacta 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   surface. These proteins are necessary for erythrocyte invasion by the
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
   RESA and FIRA have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New malaria vaccines - contains cysteine-rich DBL family protein binding domains homologous domains of the Duffy and sialic acid binding proteins
sequence coding RESA (N60472) or FIRA (N60473). RESA and FIRA hantigenicity autitable for providing protective immunity against Plasmodium falciparum malarial infections. Sequence 4590 Bp. 1933 A; 437 C; 673 G; 1547 T;
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                DB 1; Length 4590;
                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                            Score 56; DB 1; Ler
Pred. No. 0.19;
0; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "no stop codon given"
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15140. .16205
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16206. .17552
                                                                                                                                                                                                7.8%;
52.1%;
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/number=
                                                                                                                                                                                                                                                                   Conservative
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07-JUN-1995; US-487826.
(USSH ) US DEPT HEALTH
Chitnis C, Miller LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
                                                                                                                                                                                                                              Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wellems TE;
WPI; 97-05231/05.
P-PSDB; W22475.
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                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI: 98-250977/22.
Controlling phytopathogenic organisms with non-pathogenic Pythium Lisolate - for control of damping off caused by Pythium claim 17; Page 30; 41pp; English.
This is a partial nucleotide sequence of the mitochondrial DNA from a Pythium oligandrum isolate 23-5. Nucleotide sequences which are inverted repeats, flanked by PstI restriction sites from mitochondrial DNA from various P. oligandrum isolates are shown in V29576 to V29583. These Pythium isolate sequences are non-pathogenic and can be used in a method for controlling phytopathogenic organisms where the organisms are method for controlling phytopathogenic organisms where the organisms are
parasite. This sequence can be used in the compositions of the invention. The compositions are for the treatment and prevention of malaria, and comprise either a nucleotide sequence or encoded polypeptide of the var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of genes having homology with conserved regions of DABP and SABP. The compositions are used for the treatment and prevention of malaria. They are also used in the preparation of vaccines for inducing a protective immune response in a mammal to Plasmodium merozoites (especially Plasmodium faliciparum or Plasmodium vivax).

Sequence 19124 BP; 7824 A; 2190 C; 2790 G; 6320 T;
                                                                                                                                                                                                                                                                                                                                                                                                1264 ATTATAATATGTAAATTATTAATAAATATATTTGTATAACATACAGGCTAAAGAAAAC 1323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 tgttctgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatactaacagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pythium oligandrum isolate 23-5 mitochondrial DNA partial seque Pythium oligandrum; phytopathogenic; mitochondrial DNA; fungus; soil saprophyte; pathogen; tomato; mycotoxic; plant protection;
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/note= "unigue fragment claimed in claim 19"
                                                                                                                                                                                                                                                             Score 56; DB 1; Length 19124;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                            0; Mismatches 180; Indels
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                                                                                                                                                                                                                                                             7.8%;
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                                                                                                                                                                                                                                                                                                            Matches 164; Conservative
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17-OCT-1996; US-731722.
(UYFL.) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                      Best Local Similarity
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04-SEP-1998
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Gaps

Mismatches 108;

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118;

Matches

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other soil-borne pathogens), particularly for protecting plants (seedlings, transplants or vegetable crops such as tomatols gathist damping off, especially after transplanting into open fields. The isolate sequences are useful as sources of probes for identification of particular isolates. The isolates are widely distributed in mature, with a similar ecology to pathogenic species. They produce large quantities of cospore inoculum on liquid or solid substrates and are tolerant of several commonly used fundicides. A single application at the greenhouse stage will protect plants after transplanting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrella burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease claim 1; Page 801-831; 1128pp; English.

X20248 to X20402 represent polynucleotide sequences isolated from portable burgdorfer! (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of blosynthetic products, e.g. enzymes. Borrella belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrella causes epidemic and
                                                                                                                                                                                                                                                                                                                                                                 595 TATTGAAGAATTTCTTATAACTACTATTAAAGATTTATAGGATCTACTGTATAAATCCAG 536
                                                                                                                                                                                                                                                                                                                                                                                                         109 aagatttttaaaaaaatgtataaaattatattattcatgatttttcatacatttgattt 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi polynucleotide sequence #4.

Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
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                                                                                                                                                                                                                                           7.5%; Score 54.2; DB 1;
59.3%; Pred. No. 0.38;
iive 0; Mismatches 73;
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                                                                                                                                                                                                                                                              Best Local Similarity 59.3
Matches 112; Conservative
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22-JUL-1997; US-053377
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WO9858943-Al
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Length 53585;

Score 53.2; DB 1; Pred. No. 0.46;

7.4%;

Query Match Best Local Similarity

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                                                                               18 aaacataacatggatatctccttaccaatcatactaattattttgggttaaatattaatc 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant DNA molecule expressing mammalian erythropoietin useful to transform cell lines, and for gene therapy, e.g. of canaemia and other red blood cell disorders claim 7; Page 59-60; 84pp; English. Human apolipoprotein B (apoB) scaffold attachment region (SAR) element clones RN32 (731530) and RN10 (731531) respectively carry the 3; human apoB SAR element and the distal 1212 bp 5; human apoB SAR element and the special special proximal sequence. These SAR elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAR element and 1317 by proximal sequence. These SAR elements co-map with the boundaries of the human apoB gene chromatin domain. A novel recombinant DNA molecule adapted for transfection of a host cell comprises an erythropoietin (EPO) cDNA (131529) or genomic clone (131512) operably linked to an expression control sequence and to the 5' and 3' SAR elements. The SAR elements increase expression of the recombinant EPO in stable, long-term
                                                                                                                                                           190 taatttettaaaaaatgttgeaagaeacttattagaeatagtettgttetgtttaeaaaa
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Human 3' apolipoprotein B SAR element clone Rh32
Erythropoietin; EPO; anaemia; gene therapy; vecto
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                                                                                                                                                                                                                                                                                                                                                                             BP.
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Sequence 605 BP; 27
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19-DEC-1994; US-358918.
(CANG-) CANGENE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic animal; ss.
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T31530
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Orpinomyces cellulase CelB cDNA
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/note= "Claim
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Best Local Similarity 49.8
Matches 132; Conservative
                   09-APR-1998.
03-OCT-1997; U18008
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03-OCT-1997; U18008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrella burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease and therapy of infections, particularly Lyme disease Claim 1: Page 851-867; 1128pp; English X20248 to X20402 represent polynucleotide sequences isolated from Borrella burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, charctisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrella belongs to a family of motile, spiral-shaped bacterial called Spirochetes. Spirochetes are pathogenic in humans and Borrella causes epidemic and endemic relapsing fever, and Lyme borrellosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 cttaaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattc 255
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                                                                                                                                          04-MAY11939 (11130 cm.c.),

Borrella burgdorferi polynucleotide sequence #6.

Borrella burgdorferi; splrochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borrellosis; infection; diagnosis; characterisation; detection; diagnosis; characterisation; diagnosis; characterisation; detection; diagnosis; characterisation; detection; diagnosis; characterisation; detection; diagnosis; characterisation; diagnosis; characterisation; detection; diagnosis; characterisation; diagnosis; characterisation; diagnosis; characterisation; detection; diagnosis; characterisation; diagnosis; diagnosis; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3596 G;
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Orpinomyces cellulase CelB cDNA.
Cellulase: endoglucanase; CelB gene; ds
Orpinomyces sp. strain PC-2.
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69. 1484
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/note= "Claim 5"
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                                                                                     X20253 standard; DNA; 26811 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMA-) HUMAN GENOME SCI INC
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                  18-JUN-1998; U12764.
03-SEP-1997; US-057483.
20-JUN-1997; US-050359.
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1621 AAATATATACATAAACAAAAGTAAAAATTAAAAATTTTTAGTATTGTATAAATTTTATT 1680
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                                                                                                                                                                         New recombinant DNA encoding Orpinomyces cellulase protein - useful for, e.g. producing recombinant Orpinomyces cellulase in host cell claim 5; Page 38-40; 69pp; English.

This cDNA clone includes a claimed coding region for cellulase celB (see W56742) of the anaerobic bovine rumen fungus Orpinomyces sp. PC-2. It was obtained by screening a PC-2 cDNA library for clones
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                                                                                                                                                                                                                                                                                                                                                                        active on remazol brilliant blue-carboxymethylcellulose. The encoded cellulase has endoglucanase, but not cellobiohydrolase, activity. CelA and celC genes (see V29472-73), also obtained from Orpinomyces sp. PC-2, encode cellulases having both activities (see W56738-39). Recombinant DNA molecules encoding Orpinomyces cellulase proteins are claimed, as well as recombinant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus, Trichoderma reesei, Pichia, Penicillium, Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or Bacillus, and amethod for producing recombinant cellulase culturing these host cells.
Sequence 1826 BP; 654 A; 236 C; 313 G; 623 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52.2; DB 1; Length 1826;
Pred. No. 0.76;
0; Mismatches 133; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      selected from Saccharomyces cerevisiae, Escherichia coli
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Orplnomyces sp. strain PC-2.
Location/Qualifiers
CDS 69. .1484
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04-0CT-1996; US-027883.
(UYGE-) UNIV GEORGIA RES FOUND INC.
Chen H, Li X, Ljungdahl LG;
WPI: 98-240096/21.
P-PSDB: W56742.
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(UYGE-) UNIV GEORGIA RES FOUND INC
Chen H, Li X, Ljungdahl LG;
WPI; 98-240096/21.
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for, e.g. producing recombinant Orpinomyces cellulase in host cell
Claim 5; Page 38-40; 69pp; English.
This cohna clone includes a claimed coding region for cellulase celB
(see W56742) of the anaerobic bowine rumen fungus Orpinomyces sp.
PC-2. It was obtained by screening a PC-2 cDNA library for clones
c active on remazol brilliant blue-carboxymethylcellulose. The
encoded cellulase has endoglucanase, but not cellobiohydrolase,
c activity. CelA and celC genes (see V29472-73), also obtained from
C Orpinomyces sp. PC-2, encode cellulases having both activities
C see W56738-39. Recombinant DNA molecules encoding Orpinomyces
C claulase proteins are claimed, as well as recombinant cells
c selected from Saccharomyces cerevisiae, Escherichia cellulase
C Spergillus, Trichoderma reesei, Pichia, Penicillium, Streptomyces
or Baccillus, and a method for producing recombinant cellulase by
C culturing these host cells.
Sequence 1826 BP; 654 A; 236 C; 313 G; 623 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52.2; DB 1;
Pred. No. 0.76;
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1. .1935
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/product= Xylanase.
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Neocallimastix patriciarum.
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feedstock; rumen; plant fibr
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Best Local Similarity 49.8
Matches 132; Conservative
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01-APR-1993; AU-008100
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hydrolysis of xylan.
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2130 AAAAATTAAAATGTAAAAGTTTAAAAATACAAATTTGTAAGAAAAATAAAGAATTATAA 2189
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                                                                                                                                                                                                                                                                                                                         138 tattattcatgatttttcatacatttgattttgataa--taaatatatttttttaattt 195
                                                                                                                                                                                                                                                                                                                                                                   The CDNA sequence encoding the carbamoyl-phosphate-transferase II (CPSII) of Plasmodium falciparum was determined. The CDNA encodes a profein that includes 2 insert sequences not found in other CPSII proteins. The first separates the putative structural subdomain and the glutaminase subdomain of the glutaminase subdomain of the glutamine-amidotransferase subunit of CPSII, while the second separates 2 ATP binding subdomains of the
                                                                                                                                                                                                                                 Gaps
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and paper industry, for treating bagasse for more efficient disposal or for the treatment of feedstock to improve nutritional value. Genetically modified xylanase genes can also be used for the modification of rumen bacteria to improve plant fibre utilisation by
                                                                                                                                                                                                                                                                            aaacataacatggatatctccttaccaatcatactaattattttgggttaaatattaatc 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 cttaaaaaaatgttgcaagacacttattagacatagtcttgttctgtttacaaaagcattc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding carbamoyl phosphate synthetase II - isolated from Plasmodium falciparum, used to develop prods. for the treatment of malaria.
Disclosure: Page 6-16; 31pp; English.
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                                                                                                                                                                                  Length 2503;
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49.6%; Pred. No. 0.76;
.ive 0; Mismatches 135; Indels
                                                                                                                   704 T;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1994 (first entry)
Carbamoyl-phosphate-synthetase II.
Carbamoyl-phosphate-synthetase II; CPSII; psCPSII gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1232 G;
                                                                                                                                                                                                                               0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2310 AAAAATTATGAAAATTTTAAATATAAAAATTAAAAATA 2348
                                                                                                                   517 G;
                                                                                                                                                                                2; DB 1;
0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atcatttaatacattaaaaaatatttaatactaacagta
                                                                                                                                                                                Score 52.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            774 C;
                                                                                                                   389 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNIX ) UNISEARCH LTD.
Flores MV, Osullivan WJ, Stewart TS;
WPI; 94-200271/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1226. .8401
/*tag= a
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                                                                                                                   893 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPSa and CPSb
                                                                                                                                                                                  Query Match 7.3%;
Best Local Similarity 51.6%;
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 062924/c
ID 062924 standard; cDNA; 8920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1993; AU0617.
03-DEC-1992; AU-006206.
16-DEC-1992; AU-006380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
                                                                                                                   2503 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                       Ouery Match
• Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malaria; ss
                                                                                              ruminants.
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                                                                                                                        Sequence
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Recombinant DNA molecule expressing mammalian erythropoletin - weful to transform cell lines, and for gene therapy, e.g. of anaemia and other red blood cell disorders.

Claim 7: Page 59-60; 84pp; English.

Claim 7: Page 59-60; 64pp; Carry the 3' An element and Bage 6 penetrs and Comparing 6 penetrs and Colone (731532) or penably linked to an expression control capped end to the 5' and 3' SAR elements. The SAR elements

Colored Page 6 penetrs and Colone (731532) penably linked to an expression control capped end to the 5' and 3' SAR elements. The SAR elements

Colored Page 6 penable 6 penable 7 penable
                                                                                                                                                167
                                                                                                                                                                                                                                                                                                                                                                                                                                        287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 ttttgataataaatatatttttttaatttcttaaaaaaatgttgcaagacacttattaga 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 TAATTATAAATACTTTAATTATAAAATATGTAATTATAAATACTTTATAAAATATGTAAT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 TATAAAATATGTAATTATAAACATTTTAATTATAAAATATGTAATTAT -- AAACATTTTA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catagtottgttotgtttacaaaagcattcatcatttaatacattaaaaaatatttaata 285
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   aaagattttttaaaaaaatgtataaaattatattattcatgattttcatacatttgatt
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                                                                    717 ATATTTATGTTTAAAATTTTATAAATTTACATATACAAGTTCATTTTTCATATGTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-1996 (first entry)
Human 3' apolipoprotein B SAR element clone Rh32.
Erythropoietin; EPO; anaemia; gene therapy; vector; scaffold attachment region; SAR element; apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 aacagtagaatcttcttgtgagtggtgt 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537 AATTATAGGAACCACAATATTGGGGAGT 510
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Sequence 605 BP; 278 A;
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T31530 standard; cDNA; 605
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Matches 134; Conservative
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19-DEC-1994; US-358918.
(CANG-) CANGENE CORP.
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New gene encoding Plasmodium falciparum 140 kD antigen - and new fusion Disclosure; age 9; 18pp; german. proteins, transformed cells and antibodies, useful in malaria vaccines;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis, etc.

The 140 kD antigen of Plasmodium falciparum merozoites encoded by this sequence can be used in malaria vaccines, and antibodies raised against it are useful in passive immuno-prophylaxis. The antibodies, nucleic acids and proteins are also useful as diagnostic agents, and the antibodies may be used for the recovery of high-purity proteins. See also N81155-56.

Sequence 3975 BP; 1690 A; 393 C; 575 G; 1317 T;
Gaps
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                                                                                                                                                                                                                             vaccine; 140 kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                           07-NOV-1990 (first entry)
Malaria-specific gene encoding 140kD antigen
CDNA clone 140-1; ss; malaria; vaccine; 140 l
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51.8; DB Pred. No. 0.85; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1987; DE-708783.
04-DEC-1987; DE-741057.
(BEHW) Behringwerke AG.
Knapp B, Hundt E, Enders B, Kupper H;
WPI; 88-272384/39.
                                                                                                                                                                                                                                                              ocation/Qualifiers
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/label=exon II
1455. 1595
/*tag= c
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/label=exon IV
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/label=exon
488. .1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                 721. .3705
                                                                                                                                                             N81157 standard; DNA; 3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                286 ctaacagtagaat 298
                                                                              210 ATTATAAATATT 198
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RESULT

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Recombinant vector encoding hybrid Ompa protein of Salmonella for prodn. of Orally-administered malaria vaccines
for prodn. of Orally-administered malaria vaccines
for prodn. of Orally-administered malaria vaccines
To construct pompa-5. pugle-SERP which carries the complete SERP gene
on a 5.8 kb XbaI fragment (Knapp et al., Mol. Biochem. Parasitol. 32
(1989), 73-84) was digested with KpnI and PStI. A 1.3 kb DNA fragment
(see features) was isolated and ligated into the respective sites of
pSK vectors. Subcloning of the SERP fragment into pSK was performed
in order to create the correct translational reading frame at the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SERP coding region. The resulting plasmid pSK SERP was 1th Smal and KpnI, the 1.3 kb fragment was isolated and the respective sites of pHSI64L. d pomper 7 both encode 451 amino acids of the SERP antigen, 3975 BP; 1690 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note- "1.3 kb DNA fragment isolated by KpnI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pOmpA-5) or
fragment used
                                                                                              SERP gene.
Antigen; pHS164-L; SERP; malaria; pOmpA-5; pOmpA-7; ss.
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BEHW ) BEHRINGWERKE AG.
chorr J. Knapp B. Hundt E. Kupper H. Amann E;
PI; 92-089689/12.
                                                                                                                                                            Location/Qualiflers
302. 3708
/*tag a
/product SERP_antigen
302. 335
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022999
ID 022999; standard; DNA; 3975 BP. AC 022999; DT 15-JUL-1992 (first entry)
DE SERP gene.
KW Antigen; pHS164-L; SERP; malaria
OF plasmodium falciparum.
FH Key
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87 aagatattaattaagaaattaaaagattttttaaaaaaatgtataaaaattatattca 146

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Gaps

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92; Indels

Query Match

7.2%; Score 51.8; DB 1;
Best Local Similarity 53.8%; Pred. No. 0.85;
Matches 107; Conservative 0; Mismatches 92;

Length 3975;

Search completed: September 2, 2000, 02:08:21 Job time: 9270 sec

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AC005504 Plasmodiu
AC004157 Plasmodiu
AC008576 Homo sapi
AC026640 Homo sapi
AC013820 Homo sapi
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ACO06278 Plasmodiu
AL142826 Anopheles
AL139177 Homo sapi
ACO06069 Human DNA
AJ223323 Saccharom
ACO06069 Homo sapi
ACO06269 Homo sapi
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ACO11212 Homo sapi
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AC009277 Homo sapi
M33862 Dictyosteli
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U87514 Dictyostel
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J01533 Yeast (S.ce
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AC006278
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1 agatcaaactcacatccaaa.....gtttttgaagtataaagatg 719
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          OM nucleic - nucleic search, using sw model
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us-09-464-528-16.rge

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AC031982 Homo sapi X54011 D.telssieri AC009563 Homo sapi AC008206 Drosophil AC011919 Homo sapi AC012153 Homo sapi AC012153 Homo sapi AC011212 Homo sapi AC011212 Homo sapi AC011115 Homo sapi AC011115 Homo sapi AC011115 Homo sapi AC011115 Homo sapi AC01118 Homo sapi AC01118 Homo sapi AC01118 Homo sapi AC01398 Saccharomyc AC007708 Homo sapi AC01366 Homo sapi AC022266 Homo sapi AC022266 Homo sapi AC022266 Homo sapi	PRI 23-NOV-1999 352A20 on chromosome similar to yeast, bacterial, nes, and a gene coding for an sin. Contains ESTS, STSS and ara; Vertebrata; Mammalia; linidae; Homo.	Direct Submission L Submitted (07-MAY-1998) sanger.ac.uk/HGP/Chr6/) Sanger Centre, Hinxton, Cambridgeahire, Canglo 15A, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 18, 1998 this sequence version replaced gi:2909620. IMPORTAMY: This sequence is the entire insert of clone 352A20. IMPORTAMY: This sequence is the entire insert of clone 352A20. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre chromosome 6 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/ This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 352A20 is at 1 in this sequence. The true right end of clone 352A20 is at 144759 35A20 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/. 1.144759
AC031982 AC008620 AC009653 AC009653 AC018206 AC010178 AC010178 AC011212 AC011212 AC011212 AC011212 AC011212 AC01115 SCENTCG07 AC001398 AC001398 AC001398 AC001398 AC001398 AC001398 AC001398 AC001398 AC001398 AC001398	HS352A20 144759 bp DNA PRI Homo sapiens DNA sequence from PAC 352A20 on chroms of the content of	Direct Submission Submission Submitted (07-MAY-1998) sanger.ac.uk/HGP/Chr6/) San Submitted (07-MAY-1998), sanger.ac.uk/HGP/Chr6/) San Hunxton, Cambridgeshire, CB10 15A, UK. B-mail enquibunguery@sanger ac.uk Clone requests: clonerequesty Name 18, 1998 this sequence version replaced gi: Om May 18, 1998 this sequence version replaced gi: Obving sequence assembly data is compared from over Where differences are found these are annotated as Where differences are found the sequence variations annotated may not be found in the sequence responding to the overlapping clone name variations annotated may not be found in the sequence variations annotated from part of bacterial human chromosome 6, constructed by the Sanger Centimapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/ This sequence has been finished according to sequence as follows. An attempt is made to resolve all sequence is ambiguous, there is an annotation using feature key. The true right end of clone 352A20 is at 1 in this frue right end of clone 352A20 is at 1 in this feature key. For further details see http://bacpac.med.buffalo. 1. 144759 /Organism="Homo sapiens"
68879 72 AK 287311 59 AK 287731 59 AK 216406 57 AK 216406 57 AK 2173693 57 AK 2173693 59 AK 217369 8 SCI 1398 9 SCI 1398	HS352A20 144759 bp DNA Homo sapiens DNA sequence foquation and sime mold hypother aldehyde dehydrogenase fami GSSs, complete sequence. ALO21939 1 GI:3135969 HTG; aldehyde dehydrogenase human apiens Eukaryota; Metazoa; Chordate Eutheria; Primates; Catarrhiphilips, S.	Direct Submission Submitted (07-MAY-1998) sanger.ac Hinxton, Cambridgeshire, CB10 1sA humquery8aanger ac.uk Clone reque- hummquery8aanger ac.uk Clone reque- humber 18, 1998 this sequence ver. NAMPARY: This sequence is the e- Buring sequence assembly data is where differences are found these corresponding to the overlapping variations annotated may not be for corresponding to the overlapping variations annotated may not be for variations annotated may not be for corresponding to the overlapping variations annotated from mapping sequence was generated from mapping group. Further informatio http://www.sanger.ac.uk/HGP/Chr6/ This sequence has been finished a ss follows. An attempt is made to such as compressions and repeats, annotated human repeat sequence e sequence is ambiguous, there is a feature key. The true left end of clone 352A20 The true right end of clone 352A20 The true right end of clone 352A20 The true right end of clone 352A20 The true left end by the group of For further details see http://ba Location/Qualifiers 1. 144759
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0 0 000 000 00 0 000000000000000000000	RESULT 1 HS352A20 LOCUS DEFINITION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT

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note="L1MA4A repeat: matches 941. .1046 of consensus"
                                                                                                                                                                                                           1362. 1544
/note="LiPB3 repeat: matches 640. .811 of consensus"
1546. 1836
/note="Alugg repeat: matches 299. .1 of consensus"
1839. .1937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 763. .8945
note="AluY repeat: matches 300. .104 of consensus;
ncomplete repeat"

    211
    /note="AluSc repeat: matches 77. .285 of consensus;
incomplete repeat."

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 955. .9012
note="AluYb8 repeat: matches 27. .83 of consensus;
ncomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 330. .394 of consensus"
                                                                                                                                                                                                                                                                                                                                                       448. .2745
note="AluJb repeat: matches 3. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                       1863. .4153

Anote-"AluSq repeat: matches 1. .293 of consensus"

1897. .4960

Anote-"MIRZ repeat: matches 80. .146 of consensus"
                                                                                                                                                                                    562. 959
/note="AluSc repeat: matches 1. 299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              495. 9794
note="Alujo repeat: matches 1. 297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"AluSx repeat; matches 1. .296 of consensus"
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17481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 1. .300 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345. ./04/
note="AluSq repeat: matches 303. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197. .luusa
note-"Alusx repeat: matches 1. .301 of consensus"
1019. .11210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9337. .2902
Note="Allog repeat: matches 296. .1 of consensus"
0246. 30393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3302. .13473
note="MER5B repeat: matches 1. .178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluJo repeat: matches 1. .302 of consensus" 7715. .18093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ote "MIR repeat: matches 178. .66 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 4. .361 of consensus"
                                                                                                                                                34. .392
note="MER45 repeat: matches 4. .62 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .uY repeat: matches 301. .l of consensus"
4497
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15077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note-"MIR repeat: matches 7. .199 of consensus"
1212. .11507
/chromosome="6"
/map="q24.1-25.1"
/clone="RP3-352A20"
/clone=lib="RPCI-3"
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73705. 34079

/note="THEIB repeat: matches 364. 1 of consensus" 35428. 35475

/note="8 of mer 98 % conserved" 36948. 37247

/note="AluSx repeat: matches 1. 302 of consensus" 37293. 37593

/note="AluSx repeat: matches 1. 301 of consensus" 37774. 37912

/note="MIR repeat: matches 259. 119 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="LIPAl3 repeat: matches 896. .463 of consensus"
1126. .44487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Alusq repeat; matches 1. .299 of consensus"
8446. .48703
note="MER21A repeat; matches 917. .677 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8706. .49238
note="MER21A repeat: matches 568. .11 of consensus"
9308. .49633
note="MER1B repeat: matches 332. .1 of consensus"
60331. .50567
of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 146. .108 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19027. 39331

/note="Alucg repeat: matches 303. .1 of consensus"

12819. 43105

/note="Alusx repeat: matches 1. .299 of consensus"

13529. 43567

/note="MIR2 repeat: matches 146. .108 of consensus"

15579. 44043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .64 of consensus;
                                       .494 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4814. 44924
note="MIR repeat: matches 133. .230 of consensus"
5229. 45528
note="Alusx repeat: matches 300. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSq repeat: matches 132. .1 of consensus;
                                                                                                                 note-"Alusc repeat: matches 299. .1 of consensus"
1737. .32032
note-"Alujo repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                        omplement(37971. .38348)
note="match: STS G13944"
8284. .38561
note="Alujo repeat: matches 302. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ote="THEIC repeat: matches 371. .4 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1 of consensus"
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note="AluJb repeat: matches 294. .1 of consensus"
1996. .52317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4466. 54771
note="AluSq repeat: matches 303. .1 of consensus"
4792. 54871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Icomplete repeat"
1147. 47300
ote="MIR2 repeat: matches 2. .145 of consensus"
149- 47547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .134 of consensus'
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                                                                            . 1 of
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. 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6555. 46844
holde Alujb repeat: matches 290.
6905. 4680
note Alujo repeat: matches 133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1MB6 repeat: matches 920.
note-"LOR1 repeat: matches 139.
                                       matches 245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 121.
5671. .55874
                                                                            301.
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4379. .54458
                                  note="LOR1 repeat:
1006. 31314
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647. 50937
                                                                                              1416. .31711
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Surren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Braun, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, C., Kann, L., Karatas, A., Horton, L., Howland, J.C., Johnson, R., Mocdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC011212 153267 bp DNA HTG 12-MAR-2000
Homo sapiens clone RP11-3N16, WORKING DRAFT SEQUENCE, 22 unordered
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                                                                                                                                                                                                                                                                                                                                                 113389 TTTTTATATATATAAATATATTTTAT-ATATATTTTTTTATATATATATATATATATTTT 113447
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                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                      .157 of consensus;
                                                                                                            incomplete repeat"
$293. .58400
/note-*AluSq repeat: matches 108. .1 of consensus;
incomplete repeat"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 153267)
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens, clone RP11-3N16
Unpublished
                                                                                    matches 302.
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Pred. No. 0.11;
0; Mismatches 105;
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                57780. .58075
/note="Alusx repeat: m
58145. .58288
/note="Alusp repeat: m
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incomplete repeat"
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                                                                                                                                                                                                                                                                                                       isists of 22 contigs. The true order of the pleces not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                     rbitrary, Gaps between the contigs are represented as us of N, but the exact sizes of the gaps are unknown
                                                                                                                                                                                                                                             Quality coverage: 3.7 in Q20 bases; agarose-fp Quality coverage: 4.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                           a 'working draft' sequence. It current
2 contigs. The true order of the pieces
                                         oof 100 bp
contig of 10109 bp in length
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13: contig of 12897 bp in length
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15535: contig of 14712 bp in length
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134718: contig of 19083 bp in length
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f 1198 bp in length
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contig of 9014 bp in length
                                                                                                                                                        Assembly program: Phrap, version 0.96073 | Consensus quality: 111839 bases at least Q40 Consensus quality: 133540 bases at least Q20 Consensus quality: 144810 bases at least Q20
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4492 bp in length
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                                                                                                                              Sequencing vector: M13; M778]
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iive 0; Mismatches 118;
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Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B.
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an,R.W., Oin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
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58642: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length.
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HTG; HTGS_PHASE1.
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* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Pred. No. 0.36;
0; Mismatches 110; Indels
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3 67462: gap of unknown length
3 82485: contig of 15023 bp in length
6 82685: gap of unknown length
6 130281: contig of 47596 bp in length.
Location/Qualifiers
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/db_xref="taxon:5833"
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289 acagtagaatcttcttgt
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HTG; HTGS_PHASE1
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# 34881 36992: contig of 2112 bp in length gap of unknown length gap of unknown length a 40003; contig of 3010 bp in length gap of unknown length length	51194: contig of 1992 by in 1992 gap of unknown length 54232: contig of 3038 bp in 1 gap of unknown length gap of unknown length	f unknown 1 g of 2551 k f unknown 1 g of 2551 k unknown 1 f unknown 1 f unknown 1	# 68510 72140: Gontig of 3631 bp in length # 72141 74177: Contig of 2037 bp in length # 74178 76657: Contig of 2480 bp in length # 76658 81120: Contig of 4463 bp in length # 76658 81120: Contig of 4463 bp in length # 81121 83944: Contig of 2824 bp in length	9ap of unknown length 9ap of unknown length 94016: contig of 5025 bp in 1 9ap of unknown length 99820: contig of 5804 bp in 1 9ap of unknown length 103739: contig of 3919 bp in 1 9ap of unknown length 110294: contig of 6555 bp in 1 9ap of unknown length	116891: contig of 6597 b gap of unknown 122399: contig of 5508 b gap of unknown 129404: contig of 7005 b gap of unknown 136213: contig of 6809 b gap of unknown 142142: contig of 6929 b gap of unknown gap of unknown 142142: contig of 6929 b	# 142143 150401: contig of 8159 bp in length app of unknown length contig of 845 bp in length app of unknown length
Db 98983 AATAATAAATATTATTAT 98966 RESULT 5 AC008576/c AC008576 349919 bp DNA HTG 18-FEB-2000 DEFINITION Homo sapiens chromosome 19 clone CTC-557J18, WORKING DRAFT SEQUENCE, 56 unordered pieces. ACCESSION AC008576 3 G1:6997021 VERWORDS HTG: HTGS_PHASE1; HTGS_DRAFT. SOURCE human		REFERENCE 2 (bases 1 to 349919) AUTHORS DOE Joint Genome Institute. TITLE Direct Submission JOURNAL Submitted (03-Aug-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA COMMENT On Feb 18, 2000 this sequence version replaced gi:6601030. Center: Joint Genome Institute	Center Code: JGI Web site: http://www.jgi.doe.govSummary Statistics Consensus quality: 269737 bases at least Q40 Consensus quality: 300872 bases at least Q30 Consensus quality: 311585 bases at least Q20 Estimated insert size: 349919; sum-of-contigs estimation Estimated insert size: 14630; agarose-fp estimation Quality coverage: 1.90x.in Q20 bases; agarose-fp estimation	**NOTE: This is a 'working draft' sequence. It currently ** NOTE: This is a 'working draft' sequence. It currently ** Consists of 6 contigs. The true of the pieces ** is not known and their order in this sequence record is ** arbitrary. Gaps between the contigs are represented as ** runs of N, but the exact sizes of the gaps are unknown. ** This record will be updated with the finished sequence ** as soon as it is available and the accession number will ** be preserved. ** 3011: contig of 3011 bp in length	unknown ler of 3572 bp of 3672 bp of 3096 be unknown ler of 2158 bp unknown ler of 2096 bp of 2076 bp	# 16003 18305: contig of 2303 bp in length # 18306 20541: contig of 236 bp in length # 20542 23415: contig of 226 bp in length # 20542 23415: contig of 2874 bp in length # 23416 25390: contig of 1975 bp in length # 25391 27927: contig of 1975 bp in length # 27928 30114: contig of 2187 bp in length # 30115 32716: contig of 2187 bp in length # 30115 32716: contig of 2187 bp in length # 30115 32716: contig of 2187 bp in length # 30115 32716: contig of 2164 bp in length # 32717 34880: contig of 2164 bp in length

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67782: gap of 100 bp
80005: contig of 12223
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                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                      COMMENT
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(bases 1 to 164119)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bown, A., Burkett, G., Empopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzbuldh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
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Howland, J. C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC026640 164119 bp DNA HTG 13-APR-2000 Homo sapiens chromosome 11 clone RP11-69K18 map 11, WORKING DRAFT SEQUENCE, 16 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164119)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-69K18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 tttgataataaatatattttttttaatttcttaaaaaaatgttgcaagacacttattagac 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 actaattattttgggttaaatattaatcattattttaagatat---taattaagaaatt 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 atagtcttgttctgtttacaaaagcattcatcatttaatacattaaaaaatatttaatac
                                                                                                                                                                                                                                                                                                                                                                                                        Length 349919;
                                                                                                                                                                                                                                                                                                                              1188 others
                                                      gap of unknown length contig of 24424 bp in length gap of unknown length contig of 31526 bp in length gap of unknown length
                                                                                                                                                                      gap of unknown length contig of 33205 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 107; Indels
                                                                                                                                                      contig of 32217 bp in length
  bp in length
                                        of 8574 bp in length
                    length
                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.8; DB 54;
Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                          /clone="CTC-557J18"
81094 c 78642 g 92256 t
of 9561
                                                                                                                                                                                                                                                  /organism="Homo saplens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                Location/Qualifiers
1. .349919
  contig
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  219973:
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  210413
                                        219974
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AUTHORS
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Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McCkan, P., McGurk, A., McKanan, K., McRheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Sancos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                    Submitted (2-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 13, 2000 this sequence version replaced 91:7284664. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 176000; agarose-fp
Insert size: 162619; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; agarose-fp
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oof 100 bp
contig of 10719 bp in length
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67682: contig of 12693 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.960731
Consensus quality: 150998 bases at least 040
Consensus quality: 158219 bases at least 030
Consensus quality: 160955 bases at least 020
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2257 bp in length
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2817 bp in length
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25705: contig of 4032 bp in length
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contig of 6178 bp in length
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2132 bp in length
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contig of 5018 bp in length
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f 1476 bp in length
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13433: con
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3285 5541: cor
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10690: co
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bp in length

FEATURES

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Center clone name:
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                                                                                                                                                         Homo sapiens
                                         AC013820/c
LOCUS
                                                                                                                                        SOURCE
                                                                  DEFINITION
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AUTHORS
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80006 80105; gap of 100 bp
80106 106669; contig of 26594 bp in length
100 106799; gap of 100 bp
106800 164119; contig of 57320 bp in length.
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                                                                                                                                             clone_lib="RPCI-11 Human Male BAC" 11 1608
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Pred. No. 0.38;
0; Mismatches 109;
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29898 c 30038 g 51215 t
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lote≃"assembl<u>y_</u>fragment"
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(5. .5541
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                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                         clone="RP11-69K18"
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Best Local Similarity 55.3
Matches 135, Conservative
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Boron, A., Colsing, Colling, S., Collymore, A., Cooke, P., Deartellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
AC013820 179510 bp DNA HTG 01-APR-2000
Homo sapiens clone RP11-21P24, WORKING DRAFT SEQUENCE, 8 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 1, 2000 this sequence version replaced gi:6573887.
                                                                                                                                                                                                                                                                                                             Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Ammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179510)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., esfaye, S., Tirrell, A., Vassiliev, H., Vo. A., Wheeler, J., Wu, X lyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., , Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 183000; agarose-fp
Insert size: 178810; sum-of-contigs
Quality coverage: 6.8 in Q20 bases; agarose-fp
Quality coverage: 7.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 175240 bases at least Q40 Consensus quality: 177804 bases at least Q30 Consensus quality: 177720 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2702 8297: contig of 5596 bp in length
8298 8397: gap of 100 bp
8398 27253: contig of 18856 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2601: contig of 2601 bp in length
1: gap.of 100 bp
8297: contig of 5596 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-21P24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1996-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C., Baldwin, J., Barna, N., Beckerly, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2602 2701: gab.nf
                                                                                                                                                           AC013820.3 GI:7382157
HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name:
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Vertebrata; Mammalia;

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Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Cohepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Forrest, C., Gage, D., Fenstor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahm, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Leboczky, J., Levine, R., Klein, J., Landers, T., Largocque, K., Leboczky, J., Levine, R., McBwan, P., McGurk, A., McKernan, R., Morbeeters, R., Meldrim, J., Landers, T., Miranda, C., Mienga, V., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierne, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P.; Spencer, B., Stange-Thomann, N., Stojanovic, Taravers, M., Trigillio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Mul., M., M., M., M., A., A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-FEB-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This record contains 55 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be generich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smit, Ā.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 846 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 882 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 870 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                869 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 871 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 872 bp in length
                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-21D18
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                                                                         Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L3985
Center clone name: 21_D_18
                                                 Eukaryota, Metazoa, Chordata,
Eutheria, Primates, Catarrhini
1 (bases 1 to 48532)
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                                 sapiens
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                                 ORGANISM
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HOMO Sapiens clone RP11-21D18, LOW-PASS SEQUENCE SAMPLING.
AC023371
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0; Mismatches 133;
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Matches 149; Conservative
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Dictyostellum discoideum CAR3 gene, promoter region.
U87514
                                                                                                                                                                                                                                                                                  /clone_11b="RPCI-11 Human Male BAC"
9672 c 9208 g 15109 t 332 others
                                                                                                                                                                                                                                                                                                                                                Score 69; DB 51; Length 48
Pred; No. 0.65;
0; Mismatches 113; Indels
                         of 882 bp in length
unknown length
of 881 bp in length
unknown length
                                                                                                                                                                              contig of 888 bp in length
gap of unknown length
contig of 887 bp in length.
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known length
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cnown length
of 900 bp in le
unknown length
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                                                                                                                                                                                                                    Location/Qualifiers
1. 48532
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-21D18"
                                                                                                                             45881: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostellum discoideum
Eukaryota; Dictyostellida; Dici
1 (bases 1 to 975)
Kimmel, A.R. and Gollop, R.
CAR3 promoter of Dictyostellum
                                                                                                                                                       46757: conti
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                                                                                                                                                                                 47645: cc
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Best Local Similarity 54.4%;
Matches 135; Conservative
                                                   43253:
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DDU87514/c
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2 (bases 1 to 975)
Kimmel,A.R. and Gollop,R.
Direct Submission
Submitted (28-JAN-1997) LCDB, NIH, 6/Bl-22, Bethesda, MD 20892, USA
Location/Qualifiers
1. 975

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE

Dictyostelium

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.lverwort.
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Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN AC006278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodlum.
1 (bases 1 to 80920)
Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Tamaki,T., Kurdi,O.B.,
                                                                                                                                                                                                                                                                                   849 TATITITITATITITATITITITITICGACTATAGATAATTATTAATTACAAAAGATAT 790
                                                                                                                                                                                                                                                                                                                                                                                                               969 TITITITITTATITICAAAAAAAAATIGATCTITITATITATITATITAATTATTATTAT 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                          295 gaatcttcttgtgagtggtgtgggagtaggcaacctggcattgaaacgagaaagagag 354
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on Mar 15, 2000 this sequence version replaced gi:6652497.

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.
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1 80920: contig of 80920 bp in length.
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                                                                                                                                                    Length 975;
                                                                                                                                                       Score 68.4; DB 33; Mength
Pred. No. 2.4;
0; Mismatches 181; Indels
/organism="Dictyostellum discoideum"/strain="Ax-3".
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Plasmodium falciparum 3D7 chromosome 12
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malaria parasite P. falciparum.
Plasmodium falciparum
                              /db_xref-"taxon:44689
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                                                                                                                                                          9.58;
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                                                     /gene="CAR3"
1. .975
                                                                                   /gene-"CAR3"
                                                                                                 83 c
                                                                                                                                                       Query Match 9.5'
Best Local Similarity 49.4
Matches 177; Conservative
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AC006278/c
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IDS ILROSOMAL NAWA; 233 ILLOSOMAL NAWA; 120 IL
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Micasono, K., Inokuchi, H., Ohyama, K. and Ozeki, H.
Nucleotide sequence of Marchantia polymorpha chloroplast DNA: a region possibly encoding three tRNAs and three proteins including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62279 CGAAGAATATTATTAAAATATTCTATAATATAGAATTATATACAAATAATATTTTT 62220
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Nucleotide sequences of chloroplast 5S ribosomal RNA from cell
suspension cultures of the liverworts Marchantia polymorpha and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 ttgattttgataataaatatattttttttaatttcttaaaaaatgttgcaagacacttat 221
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X04465 Y0086 GI:11640
165 ribosomal RNA; 235 ribosomal RNA; 55
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Marchantiophyta, Marchantiales, Marchantlaceae, Marchantia
1 (bases 1 to 121024)
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Nucleic Acids Res. 12 (1:1), 4621-4624 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68.2; DB 60;
Pred. No. 0.7;
0; Mismatches 123;
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/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/chromosome="12"
/clone="3D7",", 30321 t
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Location/Qualifiers
1. .80920
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Best Local Similarity 53.6%;
Matches 142; Conservative
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infA: initiation factor 1 secx:
                                                                   features of the chloroplast genome: comparison of
                                                                                                                                                                                                              Submitted (17-OCT-1986) K. Ohyama, Research Centre for Cell and Tissue culture, Faculty of Agriculture, Kyoto University, Kyoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpl22: homologous to E. coll L20
rpl22: homologous to E. coll L21
rpl22: homologous to E. coll L22
rpl23: homologous to E. coll L23
rpl23: homologous to E. coll L23
rpl23: homologous to E. coll L33
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mologous to E. col
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                                                                                                                                                                                                                                                                                                                                                                                                          rpoA: homologous to E.coll
rpoB: homologous to E.coll beta'
rpoCl: homologous to E.coll beta'
rpoC2: homologous to E.coll
                                                                                                                                                                                                                                                                                                                         16S rRNA 23S
                                                                                     the sequenced chloroplast genomes
Nucleic Acids Res. 19 (5), 983-995 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosomal protein genes and related genes
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homologous to E. coll S3
homologous to E. coll S4
homologous to E. coll S7
homologous to E. coll S7
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photosystem I P700
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ATPase Fl subunit beta
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                    13 (bases 1 to 121024)
Shimada, H. and Sugiura, M.
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Pukuzawa, H., Kohchi, T., Sano, T., Shirai, H., Umesono, K.,
Inokuchi, H., Ozeki, H. and Ohyama, K.
Structure and organization of Marchantia polymorpha chloroplast
genome. III. Gene organization of the large single copy region from
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ohchi,T., Ogura,Y., Umesono,K., Yamada,Y., Komano,T., Ozeki,H., and
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Umesono, K., Inokuchi, H., Shiki, Y., Takeuchi, M., Chang, Z.,
Umesono, K., Inokuchi, T., Shirai, H., Ohyama, K. and Ozeki, H.
Fukuzawa, H., Kohchi, T., Shirai, H., Ohyama, K. and Ozeki, H.
Structure and organization of Marchantia polymorpha chloroplast
genome. II. Gene organization of the large single copy region from
                                                                            Fukuzawa, H., Uchida, Y., Yamano, Y., Ohyama, K. and Komano, T.
Molecular cloning of promoters, functional in Escherichia.coli from
Choroplast DNA of a liverwort, Marchantia polymorpha
Agric. Biol. Chem. 49, 2725-2731 (1985)
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Umesono,K., Shiki,Y., Takeuchi,M., Chang,Z., Aota,S.i., Inokuchi,H.
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FEBS Lett. 185, 203-207 (1985)
G (bases I to 121024)
Olywma, K., Fukuzawa, H., Kohchi, T., Shirai, H., Sano, T., Sano, S., Umesono, K., Shiki, Y., Takeuchi, M., Chang, Z., Aota, S., Inokuchi, H.
                                                                                                                                                                                     // Zamano.Y., Kohchi.T., Fukuzawa,H., Ohyama,K. and Komano,T.
// Vucleotide sequences of chloroplast 4.5 S ribosomal RNA from a
leafy liverwort, Jungermannia subulata, and in halloid liverwort,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding sequences for chloroplast ribosomal protein S12 from the liverwort, Marchantia polymorpha, are separated far apart on the different DNa strands a strands FEBS Lett. 198, 11-15 (1986)
7 (bases 1 to 121024)
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Nature 322, 572-574 (1986)
6 (bases 1 to 121024)
Fokusawa, H., Kohchi, T., Shirai, H., Ohyama, K., Umesono, K.,
Inokuchi, H. and Ozeki, H.
nomologue of E. coli ribosomal protein S14 '
Nucleic Acids Res. 12 (24), 9551-9565 (1984)
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This close is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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                                                                                                                URF4L(same as above)
                                                                                                                                                                                                                                                                                                                                                                   Score
                                                       URF2 (same as above)
URF3 (same as above)
URF4 (same as above)
                                                                                                                                                                                                                                                  homologous to 4Fe-4S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 tttaatactaacagtagaatcttct 303
                                                                                                                                                                                                                                                                                                                             subunit of inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       African malaria mosquito.
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.6%;
Matches 142; Conservative
                                                                                                                                                                                                                               same as above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to 910)
                                                                                                                                                                       itochondrial URFC
                                     nitochondrial URF1
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DEFINITION
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VERSION
KEYWORDS
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TITLE
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TITLE
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represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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Submitted (11-FEB-2000) Genoscope - Centre National de Sequencage :
Submitted (11-FEB-2000) Genoscope - Centre National de Sequencage :
Beb 191 91006 EVRx cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Feb 16, 2000 this sequence version replaced gi:6977814.
IMPORTANT: This sequence is unfinished and does not necessarly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716 WTATAAGTAWAITWAAATWITITITATAAAWITAITATAAAATITITITWITATAATTA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  896 TAGATATAATTATTTAAATTAAAATAAAAATAATGATATTAAAATNAAWATTAAAWW 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 attttttaaaaaaatgtataaaattatattattcatgattttcatacatttgattttga 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 taataaatatatttttttttaatttcttaaaaaatgttgcaagacacttattagacatagt 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         776 ATTINIATTITITITITITITATTATATATTITIMITITIMAATATTITITITAT 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 cttgttctgtttacaaaagcattcatcatttaatacattaaaaaaatatttaatactaaca 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone R-993B13, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence will be replaced by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phage, etc.
Contig order: 3 4, 1000 N's separate segments
Contig 3: length 4694 bp.
Contig 4: length 93569 bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                               Length 910;
                                                                                                                                                                                                                                                   66 others
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 99263)
                                                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches 117;
                                                          /organism="Anopheles gambiae"
                                                                                                                                                                                                                                                294 t.
                                                                                                                                                                                                                                                                                                                                                                        Score 67.8; D
Pred. No. 2.9;
                                                                                           /strain="PEST":
/db_xref="taxon:7165"
/clone="06E14"
/clone_11b="NotreDame1"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 14 clon
PROGRESS ***, 2 ordered pieces.
Location/Qualifiers
1. .910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                                                                                          91 9
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                                                                                                                                                                                                                                                   83
C
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 123; Conservative
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source

FEATURES

BASE COUNT ORIGIN

STS

STS

STS

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requests: clonerequest@sanger.ac.uk
On Feb 7, 2000 this sequence version replaced gi:6911915.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a mail overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RP5-1108D11 The true left end of clone RP3-495O3 is at 114928 in this sequence. The true right end of clone RP5-1183121 is at 707O3 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.ur/microsoft.20
RP5-1108D11 is from the library RPCI-5 constructed at the Roswell
Park Cancer Institute by the group of Pleter de Jong. For further
details see http://bacpac.med.buffalo.edu/
                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 152209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20
                                                                                                                                                                      Submitted (13-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L2 repeat: matches 2370. .2477 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2748 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1901. 2117
/note="MIR repeat: matches 2. .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65. .657
note="LIMA2 repeat: matches 6219. .6304 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .453 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132. .755
note="12 copies 2 mer gt 100% conserved"
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/note="L2 repeat: matches 1533. 1719 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '80. 1183
'note="MLT2A repeat: matches 1. ,413 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: proteins: Tr:Q22667"
/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      678. .731
/note="MLT2A repeat: matches 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'evidence-not_experimental
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/gene="dJ1108bl1.1"
join(<3136. .3925,44920.
/gene="dJ1108bl1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP5-1108D11"
/clone_lib="RPCI-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/note="L2
                                                                                                                                              Submission
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                                                                                                                Clark, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="matching EMBL:G03454; dbsTs:STS2670; Identified using the e-PCR software (G. Schuler)" 94531. 94651
/standard_name="N57675 (RH65918 STS45848)" /note="matching EMBL:N57675; dbsTs:STS45848; Identified using the e-PCR software (G. Schuler)" 19949 c 18494 g 28472 t 1108 others
                                                                                                                                                                                                                                                                                                                                         /standard_name="z16496 (RH53488 STS20513)"
/note="matching EMBL:z16496; dbsTS:STS20513; Identified
using the e-PCR software (G. Schuler)"
79452. 7962-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4434
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ALG34419.19 GI:6933861
HTG: CAGF9; CpG island; HMG; KIAA0737; KIAA0808; TNRC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79452. .79632
/standard_name="G03454 (RH53911 STS2670)"
the accession number will be preserved.

1 4694: contig of 4694 bp in length
4695 5694: gap of 1000 bp
5695 99263: contig of 93569 bp in length.
Location/Qualifiers
1. 99263
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Pred, No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 216;
                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                           /chromosome="14"
/clone_lib="RPCI-11"
/clone="R-993B13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.3%;
Best Local Similarity 45.6%;
Matches 187; Conservative
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63

g õ 183

243

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303

RESULT 14 HS1108D11 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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/evidence-not_experimental
fproduct="dJ1108bl1.1 (novel protein similar to C. elegans
722C1.7 (Tr:Q22667) (part of protein dJ1183121.2))"
/protein_id="Cas81659.1"
/db_xref="G1:7263911"
                                                                                               translation-"TYQGQFTNGMRHGYGVRQSVPYGMAVVVRSPLRTSLSSLRSEHS"
                                                                                                               NGTVAPDSPASPASDOPALESPAIPRGGFALSLLANBEAARAPKGGGLFORGALLGY
LRRESRYSYGSOBSRYSFLKSDLSSGASDASTASLGEAAEGADEAAPFEADIDATT
LETYMGEMKNDKRSGFGVSERSSGLRYEGEMLDNLRRGYGCTTLPDGHREEGKYRHVV
LVKOTYKRMLQLKSRYROKVEHSYEGAGRAAAIARQKAEIAASRTSHAKAKAEAAEO
AALAANQESNIÄRTLARELAPDFYQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9. .7493
.te-"LIMD3 repeat: matches 7431. .7739 of consensus"

    .8083
    .ea-"LIMD3 repeat; matches 7034. ,7431 of consensus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 7249. .7419 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINC5 repeat: matches 7833. .7925 of consensus. 12799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ote"Lind repeat: matches 4351, .4825 of consensus" 358, .13529 of matches 7249, .7419 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                               of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .394 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4. 7789
te="Alusx repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :e-"L2 repeat: matches 2234. .2705 of consensus"
                                                                                                                                                                                                                                                                                                            .254 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219. .14348
| Octe="L2 repeat: matches 1995. .2139 of consensus"
| 432. .14761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6. 9363
te="MER33 repeat: matches 1. 324 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     te="AluSx repeat: matches 1. ,304 of consensus"
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                                                                                                                                                                                                                                                                                                                        33. 5845
lote-"MIR repeat: matches 25, 136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .250 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Totoe Milk repeat: matches 156. .251 of consensus 15342. .15662 (note Milk repeat: matches 1. .311 of consensus 100te Milk repeat: matches 1. .311 of consensus
                                                                                                                                                                                                                                                                                                                                                                                            consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 63. .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .64 of consensus"
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ote="MIR repeat: matches 11. .201 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .226 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                    977. .6392
note="LTR16A repeat: matches 16. .450
Omplement(5998. .6470)
note="match: GSS: Em:AQ812840"
                                                                                                                                                                                                                                                                        .252 of
                                                                                                                                                                                                                                                                                                                                                                                          .139 of
                                                                                                                                                                                                            1588. 3794 (note="3 copies 69 mer 72% conserved") 1958. 5135 (note="MIR_repeat: matches 69. .252 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09. .7083
ote="MLT1Al repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06. .7166
ote="MER94 repeat: matches 4.
                                                                                                                                                                                                                                                                                                            repeat: matches 113.
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ote="MIR repeat: matches 192.
012. .11147
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                                                                                                                                                                                                                                                                                                                                                                                        63.
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ote="MIR repeat: matches 47.
950. .11011
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te="MIR repeat: matches 8.
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5te-"AluSx re
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ote-"LIMC5 r
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note-"MIR r
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lote="MIR r
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consensus
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"note-"L2 repeat: matches 1997. .2185 of consensus"

"note-"L18999

"note-"L7816c repeat: matches 202. .384 of consensus

70267. .20585

"note-"L2 repeat: matches 2206. .2545 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 2264. 2706 of consensus*
                                                                                                                                                                                                          Thote—"Alusx repeat: matches 1. .303 of consensus" Note—"MR repeat: matches 46. .228 of consensus" Note—"MIR repeat: matches 123. .234 of consensus" note—"MIR repeat: matches 123. .234 of consensus" complement(18708. .19271)
                                                                                                                     consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ote "MER3 repeat: matches 10, .205 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat: matches 1. .296 of consensus"
5663. .15739
note="WIR repeat: matches 40. .156 of consensus"
5903. .16562
                                                                                                                                                                                    .144 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                     .247 of consensus"
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                               15903. .16262
/note="LIME3A repeat: matches 5678. .6018 of
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                                                                                                                    .310
                                                                              /note="match: GSS: Em:AQ262524"
17211. 17513
Conte="AluvBa repeat: matches 1.
complement(17463. 17840)
/note="match: GSS: Em:AQ776838"
17657. 17742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3%; Score 66.8; DB 11;
llarity 52.5%; Pred. No. 0.88;
Conservative 0; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29552 TAATAATATATATATATATATAATATATATATT 29589
                                                                                                                                                                                                                                                                                                                        note="match: GSS: Em:A0777683"
omplement(18825. .19251)
lote="match: GSS: Em:B90590"
1964. .19192
                                                                                                                                                                      05/. .1//#4
ote="MIR repeat: matches 59.
                                                                                                                                                                                                                                                                                                                  note="match: GSS: Em:AQ760123
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                                                                                                                                                                                                                                                                                                                                                                                                              ote="MIR repeat: matches 6.
                                                                 complement (16083
                                                                                                                                                                                                                                                                                                                                complement (18812
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22522. .22556
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Best Local Similarity
Matches 146; Conserv
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LOCUS MTSCAJ23 1867 bp DNA circular PLN 11-MAR-1998 DEFINITION Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, 6

MTSCAJ23 RESULT

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Thesis (1997) Dept. of Cell & Developmental Biology, University of
Rome I, Rome, ITALY
                                                                                                                                                          Trancisci, S.

Nirect Submission
Submitted (05-FEB-1998) Francisci S., Dept. of Cell and
Submitted (05-FEB-1998) Francisci S., Dept. of Moro 5 Rome,
                               transfer RNA-Asn; transfer RNA-Met; transfer RNA-Tyr; tRNA-Asn baker; yeae; tRNA-Tyr gene. tRNA-Baker's yeast.
Mitochondrion Saccharomyces cerevisiae
Mitochondrian; Fungli Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetaes; It (bases 1 to 1867)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66.6; DB 7; Length 1
Pred. No. 3.3;
0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                              rganism-"saccharomyces cerevisiae"
rganelle-"mitochondrion"
trafh-"b23-108"
b_xref-"taxon 4932"
aplotype-"ade5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anticodon=(pos:37. .39,aa:Tyr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ote="codon recognized: UAC"
roduct="tRNA-Tyr"
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oroduct="tRNA-Asn"
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/product="tRNA-Met"
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1794. 1867
/gene="tRNA-Met"
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                 GI:2879886
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Best Local Similarity 53.7%;
Matches 138; Conservative
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